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Result
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                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match Length DB
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Gapop 60.0 , Gapext 60.0
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Copyright (c) 1993 - 2003 Compugen Ltd.
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ALIGNMENTS

	COMMENT	JOURNAL MEDLINE	AUTHORS TITLE	REFERENCE	SOURCE ORGANISM	ACCESSION VERSION KEYWORDS	RESULT 1 BM694092 LOCUS DEFINITION
Coordinated Laboratory for Computational Genomics University of Iowa 375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565 Email: bento-soares@uiowa.edu Tissue Procurement: Dr. Gregg Hageman	8889548 Contact: Soares, MB	GENOME RES. 6 (9), 791-806 (1996) 97044477	Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two approaches to facilitate gene	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 282)	Homo sapiens (human) Homo sapiens	DI-E-C1-410-0-15-0-015', mxww sequence. BM694092 BM694092.1 GI:19007350 EST.	BM694092 282 bp mRNA linear EST 28-FEB-2002 UI-E-CII-afo-o-15-0-UI.rl UI-E-CII Homo sapiens cDNA clone

124 124 124 124

100.0

BM694092 BM705593 BM700705 BM7258876

BM694092 UI-E-CII-BM705993 UI-E-DW0-BM700705 UI-E-CRI-AA258876 z832a01.r

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RESULT 2
BM705593
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AUTHORS
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Coordinated Laboratory for Computational Genomics
                                              8889548
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                                                                                   Genome Res. 6 (9),
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BM705593.1 GI:19018851
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Normalization and subtraction: two appr
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                                                                                                                                                   (bases 1 to 360) naldo, M.F., Lenno
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/dev stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="U1-E-Cl1"
/note="Organ:_eye; Vector: pT7T3-Pac (Pharmacia) with a
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/mol_type="mRNA"
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Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                             ьм/700705 406 bp mRNA linear EST 28 UI-E-CR1-aei-c-03-0-UI.r1 UI-E-CR1 Homo sapiens cDNA clone UI-E-CR1-aei-c-03-0-UI 5', mRNA sequence.
                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 406)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
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375 Newton Road , 4156 MEBRF, Iowa City, IA 52242,
  Normalization and subtraction: two
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/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
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/clone="UI-E-DW0-agi-c-06-0-UI"
/tissue_type="lens"
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                   AA258876.1 GI:1894001
EST.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                           AA258876
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375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
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Fax: 319 335 9565
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                                                                                                                                                                                                                                                                                                                           CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA 237
                                                                                                                                                                                                                                               CTGC 301
sapiens (human)
sapiens
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UI-B-CRI is a normalized CDNA library containing the following tissue(s): eye anterior segment. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-off primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pag vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT).8 tail. The sequence tag for this library is AATGCCGCAT. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
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/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
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mol_type="mRNA"
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WP:ZK287.5 CE06614 ;, mRNA sequence.
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Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 430)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J. Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterstoi,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                          W38711
430 bp mRNA linear EST 15-MAY-199
zb27c08.rl Soares parathyroid tumor NbHPA Homo sapiens cDNA clone
IMAGE:304814 5' sīmilar to WP:F35G12.9 CE00978 ;, mRNA sequence.
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through the This clone is available roya
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1 (Dases 1 to 416)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP);
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primer: -28m13 rev2 ET from Amersham.
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 3.1e-54;
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1 (bases 1 to 438)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
   WashU-Merck EST
                                                                                                                               Homo sapiens
                                                                                                                                           Homo sapiens (human)
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IMAGE:786074 5' similar to WP:
                                                                                                                                                                                                                                       AA448759
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+ET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Soares parathyroid tumor_NbHPA"
/note="Organ: parathyroid gland; Vector: pT773D (Pharmacia / with a modified polylinker; Site 1: Not I; Site_2: Eco | RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="parathyroid tumor"
/dev_stage="adult"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="GDB:1248224"
/db_xref="taxon:9606"
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100.0%; Pr
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Pred. No. 3.2e-54;
                                                                                                                                                                                           438 bp mRNA linear EST U4-JUN-
fetus KD2HF8 9w Homo sapiens cDNA clone
co WP:ZK287.5 CE06614 ;, mRNA sequence.
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                     MIPS
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Local Similarity
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Ingolstaedter Landstr.1, D-85764 Neuherberg, This is the 5' sequence of the clone insert
                                                                                                                                                            Wiemann, S.)
Unpublished
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 460)
                                                                                                                     Contact: Bloecker H
                                                                                                                                                                                                                          EST (Bloecker, H.,
                                                                                                                                                                                                                                                                                                    Bloecker,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                460 bp mRNA linear
DKFZp686006155_r1 686 (synonym: hlcc3) Homo sapiens
DKFZp686006155_5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
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This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Seq primer: -26ml3 rev2 ET from Amersham
High quality sequence stop: 399.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
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Contact: Wilson RK
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/lab host="DH10B"
/clome lib="Soares total fetus Nb2HF8_9w"
/note="Vector: pT73b-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA (polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA (polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA (polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA (polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA (polylinker; Site 3: Site 3
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/mol type="mRNA"
/db_xref="GDB:5983693"
/db_xxef="taxon:9606"
/clone="IMAGE:786074"
                                                                                                                                                                                                                                                                                                Boecher, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 124; DB 9;
100.0%; Pred. No. 3.2e-54;
tive 0; Mismatches 0;
                                                                                                                                                                                                                          Boecher, M.,
                                                                                                                                                                                                                                                                                        Brandt, P., Mewes, W.,
                                                                                                                                                                                                                      Brandt, P.,
                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                  Mewes, H.W.,
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MA 02138
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Contact: Douglas Melton, Klaus H. Kaestner
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical
Dept of Molecular and Cellular Biology, 7
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Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ,M., Gibbons,M., McCann,R., Cole,R.,
, Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hiller,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,B., Ronko,I., Bennett,J., Carden, M., Carden, 
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CA948789.1 GI:27441666
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Location/Qualifiers
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                                                                                                                                                                                   Fax: 617-495-8557
                                                                                                                                                                                                                                           Tel: 617-495-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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/note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB; CDNA-collection"
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/clone="DKFZp686006155"
/tissue_type="human skeletal muscle"
/tissue_type="adult"
/dev_stage="adult"
/lab_host="DH108"
/clone_lib="686 (synonym: hlcc3)"
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/mol_type="mRNA"
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Pred. No. 3.2e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Klaus H. Kaestner, & Hiroshi Inoue
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                                                                                                                                                               Hillier, L., Lennon, G., Becker, M., Bonaldo, M. F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins M., M., Hawkins Chissoe, S., Dietrich, N., Le, N., Le, N., Mardis, E., Moore B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                     Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson
                                                                           Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          zi09g06.rl Soares fetal liver spi
clone IMAGE:430330 5' similar to
                                                                                                                           Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Email: est@watson.wustl.edu
This clone is available roy:
                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 469)
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High quality sequence stop:
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Location/Qualifiers
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Size-selected on agarose gel Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Buclid Ave., St. Louis, MO 63110, B-mail: hinoue@lingate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."
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/lab_host="DH10B"
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/db_xref="taxon:9606"
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SOURCE
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Ludwig Institute for Cancer Res
Rua Prof. Antonio Prudente 109,
                                                                                                                            l (bases 1 to 495)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                     Shotgun sequencing of the human transcriptome with ORF expressed
                                       Contact: Simpson A.J.G.
                                                                                 Proc. Natl.
                                                                                                                         Simpson, A.J.
                                                                                                                                                                                                                                            Homo sapiens (human)
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QVO-OT0030-070300-148-g06 OT0030 Homo sapiens
AW879993
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="mRNA"
/db_xref="GDB:1330099"
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                                                                  Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
S2 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalla; Eutheria, Primates; Catarrhini; Hominidae;
1 (bases 1 to 531)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,N.
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S.,
                                 Email: yongsung@mail.kribb.re.kr
Plate: 56 row: D column: 03
                                                                                                                                                             Contact: Kim YS
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K-EST0144194 S14K402 Homo
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BQ082699.1
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV0-OT0030-070
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Tel: +55-11-2704922
Fax: +55-11-2707001
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Seq primer: puc 18 forward
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             quality sequence stop:
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/note="0rgan: ovary; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning_products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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/db_xref="taxon:9606"
/dev_stage="Adult"
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E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,
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Pred. No. 3.3e-54;
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REFERENCE
AUTHORS
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                                                                                                                                    Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
Expedit Secun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
                                                                                  Email: yongsung@mail.kribb.re.kr
Plate: 5 row: A column: 10
                                                                                                                                                                                                                                                                                    Contact: Kim YS
                                                                                                                                                                                                                                                                                                                          Kim, Y.S.
21C Frontier Korean
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                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 542)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R
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K-EST0043062 S13KMS5 Homo sapiens cDNA clone S13KMS5-5-Al0 5', mRNA
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                       quality sequence stop: 542.
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/lab host="Top10F"
/clone libb"S14K402"

/lab host="Top10F"
/clone libb"S14K402"

/note="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI;
/note="Organ: Stomach; Vector: pTZ18RP1; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124
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/cell_line="K402"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 3.4e-54;
Mismatches 0;
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AUTHORS
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Query Match 100.0%;
Best Local Similarity 100.0%;
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Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 595)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                               High quality sequence stop: 595.
                                                                                                                                                                                                                                                                                                                                 Unpublished
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                                                      Plate: LLAM9587 row: o column: 16
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Location/Qualifiers
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/db_xref="taxon:9606"
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Pred. No. 3.4e-54;
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                                                                                                                                                                                                                                                                                                 DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11793 row: f column: 11
                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, N
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                              /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5313034"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/clone lib="NIH MGC 96"
/rote="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched
                                                                                                                                                                                                                                                                      Location/Qualifiers
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126 c 165 g
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_66"
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/db_xref="taxon:9606"
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Pred. No. 3.5e-54;
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Location/Qualifiers
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Plate: 4 row: C column: 07
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="S14K402~4-C07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
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Pred. No. 3.5e-54;
Mismatches 0;
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REFERENCE
AUTHORS
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ORGANISM
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BQ186247
LOCUS
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
                                                                                                                                                                                                                                                                                                                                                      Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
Seg primer: M13 REVERSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City,
Tel: 319 335 8250
Fax: 319 335 9565
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BQ186247.1 GI:20361798
EST.
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UI-E-EUI-ajn-1-03-0-UI.rl UI-E-EUI Homo sapiens
UI-E-EUI-ajn-1-03-0-UI 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coordinated Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 621)
Bonaldo, M.F., Lennon, G. and Soares, M.B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: bento-soares@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   discovery
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                   /dev_stage="fetal and adult"
/lab_host="PH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="U1E-E31"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; U1-E-E31 is a subtracted CDMA library constructed according to Bonaldo, Lennon and Soares, Genome Research,
                                                                                                                                                                 /mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-E-EJ1-ajn-1-03-0-UI"

/tissue_type="fetal eyes, lens, eye anterior secontic nerve, retina, Retina Foveal and Macular,

Choroid"
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154 c 177 g 144 t
                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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1996. First strand cDNA synthesis was primed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>,,</u>
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Pred. No. 3.5e-54;
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ACCESSION
VERSION
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CB217926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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5', mRNA sequence.
CB217926
                                                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing by: Nati
Sequencing Center (NISC)
                                                                                                                                                                                                                                                                      Seq primer: M13RP1 reverse p
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                       Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                 Plate: LLAM12898
                                                                                                                                                                                                                                                                                                                                   info@image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment, AATGCGCAT; optic nerve, CCATTAAGTG; retina, CCGGG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
/clone lib="COGENE 6E MAN"
/clone lib="COGENE 6E MAN"
/note="Vector: pAMP1; cDNA primed using oligo-dT primer,
directionally cloned into UDG sites of pAMP1. Size
selected for insert sizes ranging from 0.2-2.0 kb.
                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5795514"
                                                                                              /dev_stage="embryo, 6 weeks
/lab_host="DH10B"
                                                                                                                                       tissue_type="mandible,
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Pred. No. 3.5e-54;
); Mismatches 0;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y. Endocrine Pancreas Consortium Unoublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       سا
                                                                                                                                                                                                                                                                                                                                                                                                                Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity J
                                                                                                                                                                                                                                                                                  Library was constructed by Dr. Hiroshi Inoue I Washington University Genome Sequencing Centes obtaining a clone please contact: Dr. Hiroshi
                                                                                                                                                                                                                                                                                                                                                                                 Dept of Molecular
MA 02138
Tel: 617-495-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Other ESTs: i125c04.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BQ632594 629 bp mRNA linear EST 02-J il25c04.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6031086 similar to TR:Q9Y5M7 Q9Y5M7 RING FINGER PROTEIN. [1] ;, mRNA
                                                                                                                                                                                                   High quality sequence stop: 495.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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BQ632594.1 GI:21684112
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                                                                                                                                                                                                                                                             (hinoue@im.wustl.edu)
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                                                                                                                                                                                                                                             primer: -40RP from Gibco
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Library constructed by M. Lovett. For more information on
this library, please contact R. Tidwell (Washington
University) or visit the COGENE website at
http://hg.wustl.edu/COGENE/."

a 147 c 182 g 149 t
/clone lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-);
/note="Organ: XhoI; cDNA made by oligo-dT priming.
                                                             /clone="IMAGE:6031086"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
                                                                                                                       /organism="Homo sapiens'
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 3.5e-54;
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1 (bases 1 to 641)

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,

Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,

Hillier,L., Marra,M., Pape,D., Wylle,T., Martin,J., Blistain,A.,

Schmitt,A., Theising,B., Ritter,B., Ronko,I., Bennett,J., Cardena
,M., Glbbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,
,Jackson,Y., and Bowers,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave
MA 02138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BQ632301 641 bp mRNA linear EST 02-JUL-2002 i125c04.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6031086 3' similar to TR:Q9Y5M7 Q9Y5M7 RING FINGER PROTEIN. [1] ;, mRNA
                                                                                                                                                                                                                    Seq primer: -40UP from Gibco High quality sequence stop: 4
                                                                                                                                                                                                                                                                                        Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Endocrine Pancreas Consortium 
Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                              Tel: 617-495-1812
Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence.
                                                                                                                                                                                                                                                                                                                                                            Email: dmelton@biohp.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                              (hinoue@im.wustl.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGC 124
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XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD;
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                     /clone="IMAGE:6031086"
/tissue_type="Purified
/lab_host="DH10B"
                                                                                                                                                                                             ty sequence stop: 449.
Location/Qualifiers
                       clone
note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI),
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG714665
BG714665
BG717016F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4799834 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                   http://image.llnl.gov
Plate: LLAM10689 row: o column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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                                                                                                                                                                                                                                                                                                                                                                        quality sequence stop: 643.
Location/Qualifiers
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                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4799834"
/tissue_type="hypothalamus"
/lab_host="DH10B"
                                                              /clone lib="NIH_MGC_96"
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcg pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcg pBluescript KS+); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTVN-3' size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full locath
for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Liconstructed by M. Brownstein (NIMH/NHGRI, National
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Size-selected on agarose gel. Average insert size -1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Size-selected
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Pred. No. 3.5e-54;
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VERSION

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FEATURES

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653 bp mRNA linear EST 30-SEP-cl132b08.zl Hembase; Erythroid Precursor Cells (LCB:cl library)
Homo sapiens cDNA clone cl132b08 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 301 402 2373
Fax: 301 435 5148
Email: jm7f@nih.gov
Email: jm7f@nih.gov
The 'cl' library was constructed by Alexander Gubin, Ph.D. in the Laboratory of Chemical Biology, NIDDK, NIH. DNA Sequencing and/or analyses by National Institutes of Health Intramural Sequencing Center (NISC). More information available at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory of Chemical Biology
National Institute of Diabetes and Digestive and Kidney Diseases
Building 10, Room 9B17, National Institutes of Health, Bethesda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                     http://hembase.niddk.nih.gov
Plate: 132 row: b column: 08
Seq primer: 5' lambda-TriplEx2 Sequencing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Jeffery L. Miller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gubin, A.N., Lee, Y.T., Bouffard, G.G. and Miller, J.L. Gene Expression in Human Erythroid Precursor Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 653)
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BU665507
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/note="Organ: blood; Vector: pTriplEx2; Site_1: SfiI; Site_2: SfiI; A complementary DNA (CDNA) library from human erythroid precursor cells was constructed using SMART PCR (polymerase chain reaction) cDNA Library Construction Kit (Clontech, Palo Alto, CA) according to
                                                                                                                       /dev_stage="Precursor erythroblasts; GPA++"
/lab_host="DH5alpha"
/clone_lb="Hembase; Erythroid Precursor Ce
                                                                                                                                                                                 /tissue_type="blood"
/cell_type="Erythroid Precursor Cells"
/cell_line="Primary Culture of Periphe
Mononuclear_Cells"
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                                                                                                          library
                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="cl132b08"
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                                                                                                                                                                                                                                                                   sex="unknown"
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Pred. No. 3.5e-54;
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                                                                                                                                                                                                      of Peripheral Blood
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MEDLINE
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TITLE
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                                                                                                                                                                                                                Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Research
                                                                                                                                                                        Seq primer: M13 FORWARD
                                                                                                                                                                                                      Genetics (www.resgen.com) or from Open Biosystems
                                                                                                                                                                                                                                                                                                                                              University of Iowa Med Labs, Iowa City, 2024 University of Iowa Med Labs, Iowa City, Tel: 319 356 4866
Fax: 319 356 7171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BM979431
BM979431.1 GI:19599873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BM979431 654 bp mRNA linear EST 21-F) UI-CF-DUI-adr-f-23-0-UI.S1 UI-CF-DUI Homo sapiens cDNA clone UI-CF-DUI-adr-f-23-0-UI 3', mRNA sequence.
                                                                                                                                                        POLYA=Yes
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: McCray,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8889548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        discovery
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1 (bases 1 to 654)
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Res. 6 (9), 791-806 (1996)
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Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modifications. Briefly, reverse transcription was performed in the presence of 1 umol/L peptide nucleic acid (PNA) oligos (N-terminal)
-biotin-GTC-CAC-CCG-AAG-CTT-G-(C-terminal) and (N-terminal)-biotin-C(T/C)T-GAA-GTT-CTC-AGG-A-(C-terminal)
. Synthesized cDNA was digested with Sfil and size-selected on a 1% agarose gel (>800bp). Large-scale sequencing of the library was performed by the NIH Intramural Sequencing Center (NISC; Http://www.nisc.nih.gov)."
Http://www.nisc.nih.gov)."
/clone="UI-CF-DUI-adr-f-23-0-UI"
/tissue_type="Primary Lung Epithelial Cells"
/dev_stage="Adult"
                                                        /organism≈"Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    approaches to facilitate gene
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BU601136
LOCUS
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ORGANISM
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ORIGIN
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COMMENT

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Matches 124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Michael Brownstein Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) . DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://imagge.llnl.gov http://imagge.llnl.gov column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: NCI
                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 678)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BU601136 678 bp n
AGENCOURT 10018944 NIH MGC 142 Homo
IMAGE:6495009 5', mRNA sequence.
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                                                                                                                                                      quality sequence stop: |
Location/Qualifiers
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/clone lib="UI-CF-DU1"
/clone lib="UI-CF-DU1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-CF-DU1 is a normalized-DNA library containing the following tissue(s): Primary Lung Epithelial Cells The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this
                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              library is GGCTGTAGGC.

TAG_LIB=UI-CF-DUI

TAG_TISSUE-Lung Egithelial Cells Tissue nos 359-368

TAG_SEQ=GGCTGTAGGC"

1 56 c 127 g 198 t
/clone="IMAGE:6495009"
/tissue_type="mixed (pool of 40 RNAs)"
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Pred. No. 3.6e-54;
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sapiens cDNA clone
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RESULT 24
AI338342/c
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                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq96g03.x1 Soares_total fetus Nb2HF8 9w Homo sapiens cDNA clone IMAGE:1939252 3' similar to wF:R10A10.2 CE12670 ZINC FINGER PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AI338342
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
1 (bases 1 to 702)
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                                                                                                                                                                                                                                                                                             Insert Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
                                                                                                                                                                                                                                                                       primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185
                                                                                                                                                                                                                                                   quality sequence
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/note="Vector: pDNR-LIB; Site 1: Sfil (ggccattatggcc);
Site_2: Sfil (ggccgcttgggcc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used in cloning as follows:
5'-AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and
5'-ATTCTAGAGGCCGACGAGGGCCGACATG-dT(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the >0.5 kb
size fraction (other fractions present in NH MCC 141).
Library created in the laboratory of M. Brownstein (NIMH,
Note: this is a NH MCC Library."

129 c 160 g 178 t 26 others
                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1939252"
/clone_lib="Soares_total_fetus_Nb2HF8_9w"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                                                                            dev_stage="8-9 weeks"
                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH10B (T1-phage-resistant)"
/clone lib="NIH MGC 142"
                                                         ab_host="DH10B"
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Pred. No. 3.6e-54;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             702 bp
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8 片 Ś 밁 Ş

REFERENCE AUTHORS

SOURCE

KEYWORDS VERSION Pocus

COMMENT

JOURNAL TITLE

FEATURES

(Pharmacia) with a

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SOURCE
ORGANISM
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VERSION
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BM704660
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUBMED
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                                                                                                                                                                                                                                                            Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iow
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BM704660 706 bp mRNA linear FUI-E-CI1-afo-o-15-0-UI.r2 UI-E-CI1 Homo sapiens cDNA UI-E-CI1-afo-o-15-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGCATGCCTGTCTTAGATGTCAAGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8889548
Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Res. 6 (9),
97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 706)
                                                                                                                                                                                                     Seq primer: M13 Reverse.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                            Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                University of Iowa
375 Newton Road , 4156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BM704660.1 GI:19017918
                                                                                                                                                                                                                                                 Genetics (www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified p7773 vector. Library went through one round of normalization, and was
                       /organism="Homo sapiens"

/mol type="mRNA"

/mol type="mRNA"

/mol type="mRNA"

/db xref="ttaxon:9606"

/clone="UI-E-CI1-afo-o-15-0-UI"

/tissue type="%RPE and Choroid"

/dev stage="adult"

/dev stage="adult"

/lab host="DH108 (Life Technologies) (T1 phage resistant)"

/clone_lib="UI-E-CI1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                constructed
note="Organ: eye; Vector: pT7T3-Pac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 124; DB 9;
Pred. No. 3.6e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                MEBRF, Iowa City, IA 52242,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                             M. Bento Soares, Univeristy of Iowa
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REFERENCE
AUTHORS
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BG718227
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 715)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                  Plate: LLAM10745 row: 1 column:
                                                                                                                                                                                                                                                                                                                            Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG718227.1 GI:13997414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG718227
                                                                                                                                                                                                                                                                                           DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified polylinker; Site 1: EGOR I; Site 2: Not I; UI-E-CII is a normalized cDNA library containing the following tissue(s): RPE and Choroid. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EGOR I adaptor, digested with Not I, and cloned directionally into pTTJ-Pac vector. The oligonucleotide used to prime sequence that is located between the Not I site and the (dT)ls tail. The sequence tag for this library is ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute
/clone="IMAGE:4828198"
/lab_host="PH10B"
/clone_lib="NIH_MGC_97"
/note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                ocation/Qualifiers
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Pred. No. 3.6e-54;
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BG761806
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
TITLE
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Plate: LLCM1674 row: f column:
Plate: '''' e-mience stop: 713.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80761806 716 bp mRNA linear EST 15-M
602718011F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4841475
                                                                                                                                                                                                                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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BG761806.1 GI:14072459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
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      178
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                                                  /tissue_type="melanotic melanoma, high MDR (cell line)"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 49"
/clone_lib="NIH MGC 49"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor:
GCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CNA synthesis kit (Stratagene) and Superscript
  Library. |
a 166 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  מפ
                          using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. | "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2 2 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library." a 184 c 217 g 163 t
                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                                                                                                        one="IMAGE:4841475"
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198 g
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Pred. No. 3.6e-54;
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BG121625
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                                                                                           Matches 124;
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Best Local
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1 (bases 1 to 745)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence. —
BG121625
BG121625.1 GI:12615134
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            602351581F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4449693
                                                                                                                                                                                                                                                                                                                                                                                          DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                  nttp://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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                                       CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
                                                     CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
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Location/Qualifiers
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                                                                                                                                                    /tissue_type="adenocarcinoma, cell line"
/lab host="DH10B (phage-resistant)"
/clome_libe="NIH MGC_90"
/clome_libe="NIH MGC_90"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
a 157 c 209 g 183 t
                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                         clone="IMAGE:4449693"
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Pred. No. 3.7e-54;
Mismatches 0;
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Pred. No. 3.6e-54;
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BG766992
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DEFINITION
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BG576768
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BG576768
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BG766992
602740511F1 NIH_MGC_49
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_87"
/note="forgan: breast; Vector: pCMV-SPORT6; Site_1: Not1;
/note="forgan: breast; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Sall; Cloned unidirectionally; oligo-dT_primed.*
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
a 156 c 187 g 203 t 1 others
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'db_xref="taxon:9606"
'clone="IMAGE:4707838"
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Primates;
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Pred. No. 3.7e-54;
     754 bp n
Homo sapiens
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       cDNA clone
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                              linear
       ear EST 15-MAY-2001
IMAGE:4870251 5',
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RESULT 31
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AUTHORS
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Best Local Similarity
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603249053F1 NIH_MGC_96 Homo sapiens
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Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 767)
                                                           Homo sapiens
                                                                                                                                        mRNA sequence.
BI601470
                                                                                                                     BI601470.1 GI:15494409
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1 (Dases 1 to 754)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Location/Qualifiers
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                                                                              sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage resistant)"
/clone_lib="NIH_MCC_49"
/clone_lib="NIH_MCC_49"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI, cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/KhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Stratagene) and Superscript
ILRT (Life_Technologies). Note: this is a NIH_MGC
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db_xref="taxon:9606"
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Primates;
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Pred. No. 3.7e-54;
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                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                               Contact: Robert Strausberg, Ph.D
                                                            Unpublished
                                                                                         1 (bases 1 to 793)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                     BG111145.1 GI:12604651
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                                                                                                                                                                                                                                               602281555F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:4369332 5',
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D
cDNA Library Preparation: Michael J. Brownstein
                                                                           National Institutes of Health, Mammalian
                                                                                                                                                                        Homo sapiens (human)
                                                                                                                                                                                                                                    mRNA sequence.
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National Institutes of Health, Mammalian Gene Collection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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'db_xref="taxon:9606"
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tissue_type="hypothalamus"
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Preparation: Life Technologies, Inc.
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Pred. No. 3.7e-54;
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                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11556 row: i column: 06
                                                                                  Plate: LLAM11556 row: i column: High quality sequence stop: 795.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 797)
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10024 row: m column: 13
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
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/lab_host="DHIOB (phage-resistant)"
/clone_lib="NIH_MGC_86"
/clone_start bone; Vector: pCMV-SPORT6; Site 1: NotI;
/note="Organ: bone; Vector: pCMV-SPORT6; Site 1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.533 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC_Library."
a 187 c 218 g 187 t 1 others
organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
/clone="IMAGE:4369332"
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Pred. No. 3.7e-54;
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1 (bases 1 to 797)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     603384080F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5393131 5',
                                                                                                                                                                                                                                                                                                                                           http://image.llnl.gov
Plate: LLAM12001 row: o column:
                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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Location/Qualifiers
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/tissue_type="mammary adenocarcinoma, cell line"
/lab host="PH10B (phage-resistant)"
/clone libe"NIH_MGC 87"
/clone libe"NIH_MGC 87"
/note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally, oligo-dT primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="NIH_MGC_120"
/note="Organ: pooled pancreas and spleen; Vector:
pcMV-SPORT6; Site 1: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert site range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."
a 179 c 212 g 198 t
                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                clone="IMAGE:5393131"
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/lab_host="DH108"
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Pred. No. 3.8e-54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Sh
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incytte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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Location/Qualifiers
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National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                           /clone_lib="NIH_MGC_96"
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for the primary library contains the primary library enriched for the p
                                                                                                                                                                                                    for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Liconstructed by M. Brownstein (NIMH/NHGRI, National
                                                                                                                                                  Institutes of 183 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4793091"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue_type="hypothalamus"
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Pred. No. 3.8e-54;
Mismatches 0;
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Pred. No. 3.8e-54;
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BI457840
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                      61 AAACAAACAAGAGGACTGTGTTGTTGTTGTCTGGGGAGAATGTAATCATTCCATTCCACAACTG 120
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CDNA Library Preparation: Michael J. Brownstein (NHGRI), Sh
Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

plate: LLAMI1701 row: g column: 04
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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225
                                                                                                                                                                   Conservative
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/note="Organ: brain; Vector: pBluescriptR (modified /note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag pBluescript claim yr mimer Size_2: SalI-XhoI (gtcgag primer Size_2: SalI-XhoI (gtcgag primer); Size-selected for average insert size_2: SalI-XhoI (gtcgag primer); This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue_type="hypothalamus"
lab_host="DH10B"
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Pred. No. 3.8e-54;
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one IMAGE:5277723 5',
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Best Local Similarity
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289
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                       121 CTGC
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shira
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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603293174F1 NIH_MGC_96 Homo
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BI668735
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Location/Qualifiers
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Plate: LLAM11791 row:
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National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/tissue_type="hypothalamus"
/lab_host="DH10B"
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'db_xref="taxon:9606"
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Pred. No. 3.8e-54;
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sapiens cDNA clone
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RESULT 38

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RESULT 39
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High quality sequence stop: 679.
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
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BI828930.1 GI:15940480
                                                        mRNA sequence.
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Tissue Procurement: Life Technologies,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="NIH_MGC_119"
//note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
//note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: EccRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EccRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH MGC Library."

a 183 c 227 g 184 t 1 others
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5166790"
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Pred. No. 3.8e-54;
; Mismatches 0;
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                                                                          sapiens
                                                                          mRNA linear EST 24-J

cDNA clone IMAGE:4374443
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                                                                                            24-JAN-2001
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REFERENCE
AUTHORS
TITLE
JOURNAL
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ORGANISM
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AUTHORS
TITLE
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BG773490
                                                                                                                              VERSION
KEYWORDS
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI),
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 840)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 847)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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http://image.llnl.gov
Plate: LLAM10038 row: b column: 12
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                                                                                                                                                                   BG773490
602720212F1 NIH_MGC_97
mRNA sequence.
BG773490
                                                                                                                                                   BG773490.1 GI:14084143
                                                                                            Homo sapiens
                                                                                                               Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                         CTGC 124
                                                                                                                                                                                                                                                                                                                                                                                            219
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                       292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="NIH_MGC_96"
/clone lib="NIH_MGC_96"
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag pBluescript KS+); Site 2: SalI-XhoI (gtcgag pBluescript size 2: SalI-XhoI (gtcgag primery library enriched normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

a 191 c 232 g 198 t
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/db_xref="taxon:9606"
/clone="IMAGB:4374443"
/tissue_type="hypothalamus"
/lab_host="DH10B"
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/mol_type="mRNA"
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Pred. No. 3.8e-54;
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mo sapiens
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                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 83) NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections
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           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                        BQ876591 8584244 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGE:6192819 5', mRNA sequence.
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BQ876591.1 GI:22268599
                                                                                                                     Unpublished Contact: Robert Strausberg, Ph.D.
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/mol type="mRN"
/db xref="taxon: 9606"
/clone="1MAGE: 4837274"
/lab host="DH1DB"
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Pred. No. 3.8e-54;
Mismatches 0;
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Indels

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Gaps

0

120 381

Hominidae;

Euteleostomi;

Collection (MGC)

information can

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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI),
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
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Clone distribution: MGC clone distribution information can
cound through the I.M.A.G.E. Consortium/LLNL at:
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REFERENCE
AUTHORS
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BE747000
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                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.
plate: LLCM762 row: e column: 12
                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence. BE747000
BE747000 GI:10160992
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601580743F1 NIH MGC 9 Homo sapiens
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1 (bases 1 to 855)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
             High quality sequence stop: 767.
Location/Qualifiers
                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D
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Plate: LLAM13595 row:
                                                                                                                                                                                                                Unpublished
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ilarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5'-GACTAGTTCTAGATCGCGAGCGGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.9 kb. This is a primary : library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life
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Not1; Site 2: Sall; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
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/dev_stage="adult, 16 yr"
/lab_host="DH10B"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 3.8e-54;
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RESULT 43
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                                                                                                                                                                                                                                                                                                                               Plate: LLCM1756 row: o column: 10
High quality sequence stop: 767.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
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/lab host="DH10B (phage-resistant)"
/clome_lib="NIH_MGC_9"
/clome_lib="NIH_MGC_9"
/clome_lib="NIH_MGC_9"
/core="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2: /note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2: /note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2: /note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2: XhoI; Site_2: XhoI; Site_3: Xho
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/clone="IMAGE:4875489"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_43"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3929459"
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Pred. No. 3.8e-54;
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 856)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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603244729F1 NIH_MGC_96 Homo sap:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
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http://image.llnl.gov
Plate: LLAM11725 row: j column: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D
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                                                                                                                                                                                                                                                                                                                                              quality sequence stop: 820.
Location/Qualifiers
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/clone libe NIH_MGC_96"
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/constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

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/mol_type="mRNA"
                                                                                                                                                                                                                                                  db xref="taxon:9606"
clone="IMAGE:5287014"
                                                                                                                                                                                                            tissue_type="hypothalamus"
lab_host="DH10B"
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Pred. No. 3.8e-54;
; Mismatches 0;
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RESULT 45
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Best Local Similarity
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                                                                         Matches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
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                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11502 row: 1 column: 21
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BI757881
BI757881.1 GI:15749459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BI75788F1 NIH MGC 114 Homo sapiens cDNA clone IMAGE:5200676 5',
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 864)
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                          CGATACGTCCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA 60
 CGATACGTGCCCCATCTGCAGGGTCCAGGTCATGATGCCTGTCTTAGATGTCAAGCTGA 275
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                                                                                                                                                                 221
                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="TMAGE:5200676"
/lab_host="DH10B"
                                                                                                                                                           /note="Torgan: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                    clone_lib="NIH_MGC_114"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
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Pred. No. 3.8e-54;
                                                                          Score 124; DB 12;
Pred. No. 3.8e-54;
Mismatches 0;
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CB991438
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JOURNAL
                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                             Matches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
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 121
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                                                                                                                 AGENCOURT 13621565 NIH MGC 148 Homo sapiens cDNA clone IMAGE:30338533 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and advice from Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue Procurement: Dr. Stefan Hansson cDNA Library Preparation: Michael J. J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 886)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://image.llnl.gov
Plate: NDAM365 row: f column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGC 124
                             CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
                                                                                                   CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
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Location/Qualifiers
                                                                                                                                             Conservative
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                                                                                                                                                                                                                Library."
1 213 c
                                                                                                                                                                                                                                        directionally cloned using primer for average insert 5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-lenght clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                         /clone_lib="NIH_MGC_148"
/note="Organ: placenta; Vector: pBluescriptR; Site_1:
all-XhoI; Site_2: BamH; Library is oligo-dT primed and
                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30338533"
                                                                                                                                                                                                                                                                                                                                                                                       tissue_type="pre-eclamptic placenta"
lab_host="DH10B TonA"
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Pred. No. 3.9e-54;
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AUTHORS
TITLE
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KEYWORDS
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                                           BI759082.1 GI:15750660
                                                          BI759082
                                                                 mRNA sequence.
                                                                                 603042879F1 NIH_MGC_116
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Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4777129"
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1 CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGCCTGTCTTAGATGTCAAGCTGA
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cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 904)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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602651707F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4777129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM10630 row: m column: 02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Skn3"
/note="Torgan; skin, Vector: pcMV-SPORT6; Site_1: NotI;
/note="Torgan; skin, Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP_Library."
223 c 254 g 211 t Tothers
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Pred. No. 3.9e-54;
); Mismatches 0;
sapiens cDNA clone IMAGE:5183419 5',
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AUTHORS
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ORGANISM
                                                                                                                                                                                  KEYWORDS
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JOURNAL
                                                              AUTHORS
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 922)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _
Unpublished
Contact: Robert Strausberg, Ph.D
                                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                             BU192094 922 bp
AGENCOURT_7968580 NIH_MGC_68 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM.1457 row: m column: 20
                                                                                                                                                                                                                         5', mRNA sequence.
BU192094
                                                                                                                                                                                                    BU192094.1 GI:22706078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=morgan: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Institutes of Health,
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'db_xref="taxon:9606"
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|ab_host="DH10B"
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                                                                                                                                                                                                                                                                   IMAGE: 6011203
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Tissue Procurement: ATCC
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1. (bases 1 to 947)
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EST.
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BG111792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13200 row: h column: 20
                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="NIH MGC 68"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI
/site_2: SalI, Cloned unidirectionally. Primer: Oligo
Average insert size 1.8 kb. Library constructed by
Technologies. "
202 c 250 g 220 t 1 others
/organism="Homo sapiens"
                              Location/Qualifiers
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db_xref="taxon:9606"
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lab_host="DH10B (phage-resistant)"
clone_lib="NIH MGC 68"
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Pred. No. 3.9e-54;
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BASE COUNT
ORIGIN
Search completed: November 7, 2003, 11:54:01 Job time : 1272.21 secs
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/db xref="taxon:9606"
/clone="IMAGE:4372819"
/tissue_type="osteosarcoma, cell line"
/tissue_type="osteosarcoma, cell line"
/lab host="HIHOB (phage-resistant)"
/clone=lib="NIH_MGC_86"
/clone=lib="NIH_MGC_86"
/clone=solutionally; oligo-dT primed.
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.533 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC_Library."
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D24147	842	M94634	Y7576	9511	800	E62811	982	F30226	B209	w	91	B57146	F38373	1880	4	4472	747	7767	1794	\vdash	518	CA464071	14	37	53	AK007588	급	94	H3 Z3 81	Y71062	B20938	A9	41093	173200	Q96411	Q96415	B2045	U84098	7	
AGENCOURT	AGENCOURT	-M-EM	BY757681	AGENCOURT	L0259F11-	9a11.	602095851	602031233	GEN	BY737338	ω	\sim	N	<u>3</u>	602913971	UI-M-EM0-	UI-M-ERO-	GEN	602820877	AGENCOURT	602903365	AGENCOURT	GENCOUR	603279634	0	Mus muscu	UI-M-FBO-	ENC	UI-M-FXO-	BY710626	AGENCOURT	GENCOUR	6212	603355869	AGENCOURT	AGENCOURT	AGENCOURT	GENCOU	BY703542	•

ALIGNMENTS

AKO03963
AKO0396
AKOO396
AKOO

TITLE

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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 20-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
Group Phase I & II Team.
Analysis of the mouse transcriptome based on of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1132)
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                                                                                                                                                                                                                                                                                    further details.
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                                                                                                                                                                                                                                                                                                                                              Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
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1114 bp mRNA linear HTC 05-DEC-2002 Mus musculus 10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610005N22 product:ring finger protein 7,
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                                                                                                                                                                     physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RENGER Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

Fax:81-45-503-9216)
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Analysis of the mouse transcriptome of 60,770 full-length cDNAs
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Submitted (10-JUL-2000) Yoshihide Hayashizaki,
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                                                                                   GTTTGTGTTTATGCTTGAGGGGTTAAAAAATAGATAAACGAATGTTACAGTAACAAATAAA
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                              ATGCATTGAAAAGCCGACTCCTCCTAATCCTTTTTGTGTTGGGAGAGAGGCAAGCCGAGGC
                                        GTTTGTGTTTATGCTTGAGGGTTAAAAAATAGATAAACGAATGTTACAGTAACAAATAAA
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/clone_Tib="RIKEN full-length
/dev_stage="10 days embryo"
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/db_xref="MGI:1833659"
/db_xref="MGI:1833659"
/db_xref="taxxon:10090"
/clone="2610005N22"
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CACCCTGCTGTCATTTGCTGTGAATGAGGATTTTAACCTGCACTCAGTGAAGAGGCG

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RESULT 3
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, Alawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, I., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldareili, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
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20499374
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lev,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
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Analysis of the mouse transcriptome based on of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1084)
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/db xref="FANTOM DB:1110001M08"
/db xref="MGI:1852372"
/db xref="taxon:10090"
/clone="1110001M08"
/protein_id="BAB22666.1"
/db_xref="GI:12833796"
/db_xref="MGI:1337096"
                                                                                                                                                                                                 /tissue_type="whole body"
/clone_lib="RIKEN full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                  /note="unnamed protein product; putative
ring finger protein 7 (MGD|MGI:1337096)"
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L5. .356
                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
/mol_type="mRNA"
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Kouda, M., Owa, C.,

Aono, H.,

Suzuki, H.,

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REFERENCE
AUTHORS
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Mus musculus adult male kidney cDNA, RIKEN full-length enriched
library, clone:0610013021 product:ring finger protein 7, full
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
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                                                             TTCTCCATCTTTGACTTGGCCAGGAAGCCTGGATTGTTCAACCACTTAGTTCTAAAGAAC
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URL:http://genome.gsc.riken.go.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Hori,F., Imotani,K.,
S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K.,
Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno
H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,
Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Yoshihide Hayashizaki
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BY704214 RIKEN full-length enriched,
musculus cDNA clone 1110029M05 5', m
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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Computational Analysis of Full-Length Mouse cDNAs Compared with uman Genome Sequences Mamm. Genome. 12, 673-677 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Re 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prepare mouse tissues.
Please visit our web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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ACCTCTGGTGTGTGTGTGATACGAATGCATAGAAGAGCGAGAACACCAGAAAATGATC
                                                                           TCTGTTTAGTTTTGGGAAATTCTCTACAATTAAGATAATTTGTTAAAAATGGCCTTTCCT
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/dev_stage="18-day embryo"
/clone_lib="RIKEN full-length enriched, 18-day embryo
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COMMENT

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Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group,
Sciences Center(GSC), Yokohama Institute
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda, S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K.,
Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,
Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
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                      TGCCCTCTGTGCCAGCAGGACTGGGTAGTCCAAAGAATCGGCAAATGAGAGGTGGCCCAG
                                                                                                                                                                                GATGCCTGCCTTCGATGTCAAGCTGAAAACAAGCAAGAGGACTGTGTTCTGGGTCTTGGGGA 250
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                                                                                                    GAGTGTAACCATTCCTTCCACAACTGCTGCATGTCCCTGTGGGTGAAACAGAACAATCGC
                                                                                                                                                    GATGCCTGCCTTCGATGTCAAGCTGAAAACAAGCAAGAGGACTGTGTTGTGGTCTGGGGA
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TGCCCTCTGTGCCAGCAGGACTGGGTAGTCCAAAGAATCGGCAAATGAGAGGTGGCCCAG
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-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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/dev_stage="18-day embryo"
/clone_lib="RIKEN full-length
whole_body"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution informatifound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM14101 row: b column: 08
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 949) NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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AGENCOURT 10187674 NIH MGC 134 Mus
IMAGE:6518791 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg,
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/mol_type="mRNA"
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/clone="IMAGE:6518791"
/tissue_type="undifferentiated limb"
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/tissue_type="undifferentiated limb"
/lab_host="DH10B (phage-resistant)"
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Tissue Procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp.
cDNA Library Preparation: Invitrogen Corp.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM0041 row: p column: 12
High quality sequence stop: 678.
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National Institutes of Health, Mammalian
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/note="Vector: pCMVSport6.1; Site 2: NotI]
/note="Vector: pC
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/db_xref="taxon:10090"
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cDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                  Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
                                                                                                                                         1 (bases 1 to 1185)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                   Mus musculus (house mouse)
Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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BQ964159.1 GI:22379637
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IMAGE: 6509718 5', mRNA sequence.
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               AAAATGCATTGAAAAGCCGACTCCTCCTAATCC--TTTTTGTGTTTGGGAGAGAGAGCCAAGC
                                                         ATTGTTTGTGTTTATGCTTGAGGGTTAAAAAATAGATAAACGAATGTTACAGTAACAAAT
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                                                                                                                 GAAAATGATCTTTGTTTATCTGTACCCACGACTGTGGGGGACATTGTGTTCACAGAAGAAC
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//lab_host="DH10B (phage-resistant)"
/clone_libe="NIH_MGC_134"
/clone_tibe="NIH_MGC_134"
/note="Vector: pCMV-SPORT6.1.ccdb; Site_1: EcoRV;
/note="Vector: pCMV-SPORT6.1.ccdb; Site_1: EcoRV;
/note: Toloned unidirectionally. Primer: Oligo dT. A
insert size_1.7 kb. Constructed by ResGen, Invitro
Corp. Note: this is a NIH_MGC_Library."
a 256 c 331 g 307 t 5 others
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                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM14089 row: b column: 17
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BQ964115.1 GI:22379593
EST.
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AGENCOURT 10053663 NIH_MGC_134 Mus
IMAGE:6514192 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
                                                                                                                                                                     Similarity
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                         GTGAAACAGAACAATCGCTGCCCCTCTGTGCCAGCAGGACTGGGTAGTCCAAAGAATCGGC
                                                    AAATGAGAGGTGGCCCAGGCGCTCCTGGTGTGGTTGCTGACCCTGGACAAAAGACTAAACA
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                                                                                                                                                        Conservative
                                                                                                                                                                                                                          /organism="Mus musculus"
/mol type="mRNA"
/mol type="mRNA"
/db Xref="caxon:10090"
/db Xref="caxon:10090"
/clone="IMAGE:6514192"
/tissue_type="undifferentiated limb"
/tlab host="DH10B (phage-resistant)"
/clone lib="NIH MGC 134"
/clone lib="NIH MGC 134"
/note="Vector: pCMV-SPORT6.1.codb; Site 1: EcoRV, Site 2:
/note="Vector: pCMV-SPORT6.1.codb; Site 1: EcoRV, Site 2:
/note: tsize 1.7 kb. Constructed by ReaGen, Invitrogen
insert size 1.7 kb. Constructed by ReaGen, Invitrogen
Corp. Note: this is a NIH_MGC Library."
88 a 170 c 219 g 282 t 9 others
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies,
                                                 National Institutes of Health, Ma
Unpublished
Contact: Robert Strausberg, Ph.D.
                                                               3ukaryota, ...
Mammalia; Eutheria; Rodentia, ...
1 (bases 1 to 820)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                     Mus musculus (house
                                                                                                                                                                                                                                                              603355869F1 NIH_MGC_94 Mus musculus cDNA clone
                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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BI732003.1
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
plate: LLAM11923 row: j column: 17
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/lab_host="PHi0B (phage-resistant)"
/clone_lib="NIH_MGC 94"
/clone_lib="NIH_MGC 94"
/note="Organ: eye, Vector: pCMV-SPORT6; Site 1: NotI;
/note="Organ: eye, Vector: pCMV-SPORT6; Site 1: NotI;
/note="Organ: eye, Vector: pCMV-SPORT6; Site 1: NotI;
/note="Organ: eye, Vector: pCMV-SPORT6; Site 1: NotE; SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
a 157 c 204 g 240 t
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/db_xref="taxon:10090"
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Pred. No. 2.2e-153;
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EST.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 1079)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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National Institutes of Health, Mammalian
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Clone distribution: NCI-CGAP clone distribution information can
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                                            AGGACGGCGAGGAACCCTGCGTTTCTTCGCACTCCGGGAGCGCAGGCTCCAAGTCGG
GAGGCGACAAGATGTT-CTCTCAAGAAGTGGAACGCGGTAGCCATGTGGAGCTGGGAC 148
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                           AGGACGGCGAGGAA-CCTGCGGTCTTTCTTCGCACTCCGGGAGCGCAGGCTCCAAGTCGG
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                tissue_type="pooled lung tumors"
                                                                                                                                                                                                                                                                                                                                                                             db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                              strain="CZECH II"
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Pred. No. 6.6e-151;
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CA980368.1 GI:27513022
EST.
Mus musculus (house mous
                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 882)
                                                                                                         CA980368 882 bp
AGENCOURT 11294967 NIH MGC 164 Mus
IMAGE: 30145601 5', mRNA sequence.
                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Robert Strausberg, Ph
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   GAAAAGCCGACTCCTAATCCTTTTTGTGTTGGGA
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251 GAGTGTAACCATTCCTTCCACAACTGCTGCATGTCCCTGTGGGTGAAACAGAACAATCGC
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Tissue Procurement: Dr. David Rowe and Dr. Mina
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM0059 row: o column: 18
High quality sequence stop: 662.
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GAAAAGCCGACTCCTCCTAATCCTTTTTGTGTTTGGGAGAGAGGGCAAGCGAGGCCACCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCCCTCTGTGCCAGCAGGACTGGGTAGTCCAAAGAATCGGCAAATGAGAGGTGGCCCAG
                                                                      TTTATGCTTGAGGGTTAAAAAATAGATAAACGAATGTTACAGTAACAAATAAAATGCATT
                                                                                                  TTTATGCTTGAGGGTTAAAAAATAGATAAACGAATGTTACAGTAACAAATAAAATGCATT
                                                                                                                                                                         TTTGTTTATCTGTACCCACGACT---GGAACATTGTGTTCACAGAAGAACATTGTTTGTG
                                                                                                                                                                                                                                                                         ACCTCTGGTGTGTGTGTGATACGAATGCATAGAAGAGCGAGAACACCAGAAAATGATC
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nilarity 97.4%;
Conservative
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//clone="IMAGE:30145601"
//lab host="DH10B (phage-resistant)"
//clone="IbH="NIH_MGC 164"
//clone="Ib="NIH_MGC 164"
//clone="Vector: pCMV-SPORT6.1.ccdb; Site_1: EcoRV; Site_2:
//note="Vector: pCMV-SPORT6.1.cdb; Site_1: EcoRV; Site_2:
//clone="Vector: pCMV-SPORT6.1.cdb; Site_1: EcoRV; Site_2:
//clone-"Vector: pCMV-SPORT6.1.cdb; Maxilla and mandible, day
pooled mouse embryonic limb, maxilla and mandible, day
10.5 and 11.5 (size selected for the 0.5-1 kb fragments)
//cloned directionally, priming method: Oligo-dT. cDNA
enrichment: lk bp, Average insert size 1.8k bp. Priming
sequence: 5'GACTAGTTCTAGATCGCGAGCGGCCC(T) 3'. Tissue
contributed by, David Rowe. Library constructed by ResGen,
Invitrogen Corp."

34 a 173 c 230 g 244 t 1 others
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'db_xref="taxon:10090"
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Pred. No. 4.9e-148;
0; Mismatches 15;
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: NDAM0319 row: g column: 18
High quality sequence stop: 712.
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AGENCOURT 11350935 NIH MGC 164 Mus
IMAGE: 30245249 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CB209388.1 GI:28250951
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CGGGAGCGCAGGCTCCAAGTCGGGAGGCGACAAGATGTTCTCTCAAGAAGTGGAACGC
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                                                                                                                                               204
                                                                  Conservative
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/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_164"
/clone_lib="NIH_MGC_164"
/clone_lib="NIH_MGC_164"
/note="Vector: pCMV-SPORTG.1.ccdb; Site_1: EcoRV; Site_2:
/notl; Non-normalized full-length enriched library from
pooled mouse embryonic limb, maxilla and mandible, day
10.5 and 11.5 (size selected for the 0.5-1 kb fragments)
Cloned directionally, priming method: Oligo-dT. cDNA
enrichment: >lk bp, Average insert size 1.8k bp. Priming
sequence: 5'GACTAGTTCTAGATCGCGACCGCCCC(T) 3'. Tissue
                                                                                                                                         contributed by, David Rowe. Library constructed by ResGen,
Invitrogen Corp."
153 c 211 g 202 t 168 others
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/db_xref="taxon:10090"
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                                                                                64.9%;
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Pred. No. 6e-148;
0; Mismatches
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BY710626
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                               BY710626
BY710626.1
EST.
                                                                               BY710626

BY710626 RIKEN full-length enriched, 10 days embryo cDNA clone 2610005N22 5', mRNA sequence.
Mus musculus (house mouse)
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REFERENCE AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases t to 965)

El (bases t to 965)

Sokazaki, Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Salto, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Ouackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Dusckenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, J. E., Cousins, S., Dalla, B., Dragani, T.A., Fletcher, C. F., Forrest, A., Frazèr, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Hori,F., Imotani,K.,
S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K.,
Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno,
H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,
Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waki,K., Wa
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Please visit our web
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                            /clone lib="RIKEN full-length enriched, 10 days embryo" /clone lib="RIKEN full-length enriched, 10 days embryo" /note="Site 1: Sal1; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
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/lab_host="DH10B"
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/db_xref="taxon:100
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/mol_type="mRNA"
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TTTATGCTTGAGGGTTAAAAAATAGATAAACGAATGTTACAGTAACAAATAAAATGCATT
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
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Mus musculus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1. (bases 1 to 743)
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UI-M-FXO-cci-h-20-0-UI.rl NIH_BMAP_FXO Mus
IMAGE: 6820005 5', mRNA sequence.
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National Institutes of Health, Mammalian
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CA323814.1 GI:24541912
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                          CGACAAGATGTTCTCTCAAGAAGTGGAACGCGGTAGCCATGTGGAGCTGGGACGTTGA
                                                                                                                                                                          CGACAAGATGTTCTCTCTCAAGAAGTGGAACGCGGTAGCCATGTGGAGCTGGGACGTTGA
primer: pYX-5
                                                                                                                                                                                                                                                                                                        196
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                              /tissue_type="whole brain"
//dev stage="embryo 13.5,14.5,16.5,17.5dpc"
//lab_host="MIHUB (TI phage resistant)"
/clone_lib="NIH_BMAP_FX0"
//clone_lib="NIH_BMAP_FX0"
/note="Organ: Brain; Vector: pyx- Asc; Site_1: EcoR I;
/note="Organ: Brain; Vector: Demble strand cDNA was size fraction, ligg-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligg-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligg-dd with EcoR I adaptor, dige-sted with NotI and then cloned directionally into pyx-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
/program coordinator."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone was contributed by the Brain Molecular Anatomy Project
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/strain="C57BL/6"
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Pred. No. 6.6e-145;
0; Mismatches 1;
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BU513948.1
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM14079 row: j column: 15
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, M
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                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
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                                             Location/Qualifiers
organism="Mus musculus"
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_type="mRNA"

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/tissue_type="undifferentiated limb"
/tissue_type="undifferentiated limb"
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/clone=lib="NIH MGC_134"
/clone=lib="NIH MGC_134"
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/note="Tector: pCMV-SpNRT6.1.ccdb; Site_1: EcoRV; Site_2: pCMV-SpNRT6.1.ccdb; Site_1: EcoRV; Site_2: pCMV-SpNRT6.1.ccdb; Site_1: EcoRV; Site_2: pCMV-SpNRT6.1.ccdb; Site_1: EcoRV; Site_2: pCMV-SpNRT6.1.ccdb; Site_1: pCMV-SpN
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93.2%;
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01-M-FB0-bxz-o-08-0-UI.rl NIH_BMAP_FB0 Mus musculus cDNA
IMAGE:5715295 5', mRNA sequence.
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Tissue Procurement: Dr. James Lin, Univeristy of Iowa
Tissue Procurement: Dr. M. Bento Soares, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
This clone was contributed by the Brain Mole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
Contact: Robert Strausberg, Ph.D.
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National Institutes of Health,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
1 (bases 1 to 728)
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Mammalia; Eutheria; Rodentia; Sciurognathi, Muridae; Murinae; Mus
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//tissue_type="whole brain"
//ab_nost="pH10B (TI phage resistant)"
/lab_nost="pH10B (TI phage resistant)"
/clone lib="NIH BMAP FB0"
/clone lib="NIH BMAP FB0"
/clone lib="NIH BMAP FB0"
/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
/note="Cryan: brain; Vector: brain; Site Ibrary tagesquence located between the Not I site not I; and then interestly of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Instututes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
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/mol type="mRNA"
/strain="C57BL/6"
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                                                                                            Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new captage of the control of the control of the control of the control of the captage of the c
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

LI Nature 420, 563-573 (2002)

E 6 (bases 1 to 722)

Anakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,

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Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,

Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,

Direct Submission

Submitted (10,101-2000) Vochibida Havashizaki Tha Institute of

L. Submitted (10,101-2000) Vochibida Havashizaki Tha Institute of
                                                                                                                                                                                                                                                                                                                                                              Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

Please visit our web site (http://genome.gsc.riken.go.jp/) for
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Tahii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipaline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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             TGTGTGTGTGTGATACGAATGCATAGAAGAGCGAGAACACCAGAAAATGATCTTTGTTTA 618
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/db_xref="WGI:1892879"
/db_xref="WGI:1892879"
/db_xref="taxon:10090"
/clone="1810023A07"
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/db xref="MGI:1337096"
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/mol_type="mRNA"
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/clone_Tib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="10 day old"
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                                                                                                                                                                                                                                                                                                                                                                                           Notaset, Y., Futuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Ogato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yamanaka, I., Kayosawa, H., Yamanaka, I., Kayosawa, H., Saito, R., Suzuki, H., Yamanaka, I., Kayosawa, H., Saito, R., Yamanaka, I., Kayosawa, H., Yamanaka, I., Kayosawa, H., Saito, R., Yamanaka, I., Kayosawa, H., Saito, R., Yamanaka, Y., Ngami, A., Saitonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Gojobori, T., Bake, J.A., Brade, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Oustincich, S., Hirokawa, N., Jackson, I.J., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, Y., Kedzierski, R.M., Gough, J., Grimmond, S., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B. L., Konsaya, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B. L., Konsaya, Y., Kedzierski, R.M., King, B. L., Konsaya, Y., Kedzierski, R.M., King, B. L., Konsaya, Y., Kedzierski, R.M., Majott, D.R., Maltais, L., Marchiomi, L., McKenzie, L., Miki, P.A., Nathata, Y., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., Kayashi, M., Sandelin, R., Takenaka, Y., Taylor, M., Pertea, G., Petrea, G., Petrevsky, N., Pillai, R., Pontius, J.U., Qi, D., Rigger, M., Wahlestedt, C., Wang, Y., Rigger, L., Wahlestedt, C., Wang, Y., Wahlestedt, C., Wang, Y., Wahlestedt, C., Wang, Y., Wahlestedt, C., Wang, Y., Wang, E., Lawasawa, T., Konno, H., Nakawa, T., Konno, H., Nakawa, M., Yang, I., Yang, I., Yang, Z., Zavolan, M., Zhu, Y., Zimmer, A., M., Sakazuwe, N., Sato, K., Shizaki, T., Waki, K., Kawai, J., Aizawa, K., Yang, I., Wang, J., Yoshino, M., Waterston, R., Lander, K., Shizaki, T., Waki, K., Kawai, J., Shibata, Y., Ishidata, Y., Ishidata, Y., Ishidata, Y., Ishidata, Y., Ishidata, Y., Sato, K., Shizaki, T., Sakai, K., Sasaki, D., Shibata, Y., Sato, K., Sato, K., Sakai, K., Sasaki, N., Sakai, K., Sasaki, N., Sakai, K., Sasaki, D., Shi
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                                                                                Email: genome-res@gsc.riken.go.jp,

MRL:http://genome.gsc.riken.go.jp,

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Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Hori,F., Imotani,K.,

S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K.,

Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno

H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,

Numazaki,R., Ohno,M., Ohasto,N., Saito,R., Sakazume,N., Sano,H.,

Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,

Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
                                                                                                                                                                                                                                                                                                                                                                                 Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prepare mouse tissues.
Please visit our web
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                                                                     GTTTTGGGAAATTCTCTACAATTAAGATAATTTGTTAAAAATGGCCTTTCCTACCTCTGG
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                                                  GTTTTGGGAAATTCTCTACAATTAAGATAATTTGTTAAAAATTGGCCTTTCCTACCTCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    visit our web site (http://genome.gsc.riken.go.jp) for
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a 147 c
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/dev_stage="10 day old"
/clone_lib="RIKEN full-length enriched,
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/db_xref="taxon:10090"
/clone="1810023A07"
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Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia I
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
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                                          CCAAGTCGGGAGGCGACAAGATGTTCTCTCTCAAGAAGTGGAACGCGGTAGCCATGTGGA
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall;
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall;
Site 2: Notl; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
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/strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5319872"
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/mol_type="mRNA"
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/lab_host="DH10B"
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                                                                                                                                                                                           Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 889)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                   CB196142
CB196142.1 GI:28223462
EST.
Mus musculus (house mouse)
                                                    cDNA Library Preparation: Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDAM0039 row: n column: 23

High quality sequence stop: 718.
                                                                                                                                                                                                                                                                                                               CB196142 889 bp mRNA linear EST 05-FEB-2003
AGENCOURT 11258914 NIH MGC_135 Mus musculus cDNA clone
IMAGE:30137902 5', mRNA sequence.
                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                     Unpublished
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/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
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/lab host="DH10B [phage-resistant)"
/clone lib="NHH MGC 135"
/clone lib="NHH MGC 135"
/note="Vector: pCMVSport6.1; Site 1: BcoRV; Site 2: NotI;
/note="Vector: pCMVSport6.1; Site 1: BcoRV; Site 2: NotI;
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Pred. No. 8.8e-136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jonathan Kuo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                   GGTCTGGGGAGAGTGTAACCATTCCTTCCACAACTGCTGCATGTCCCTGTGGGTGAAACA
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//mol type="mrNA"
/db_xref="taxon:10000"
/db_xref="taxon:10000"
/clone="IMAGE:6771682"
/lab_host="DH10B (Tl-phage-resistant)"
/lab_host="DH10B (Tl-phage-resistant)"
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/clone_lib="NHH MGC 169"
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http://image.llnl.gov
plate: LLAMI1092 row: a column:
plate: TLAMI1092 row: a column:
                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 978)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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602903365F1_NCI_CGAP_Mam3
                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
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Mammalia; Eutheria;
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                                                                                                                                                                                               quality sequence stop: |
Location/Qualifiers
/tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
                                                                                    /mol_type="mRNA"
/strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
                                                                                                                                                                               1. .978
                                                                    clone="IMAGE:5032984"
                                                                                                                                                      organism="Mus musculus"
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                                        GTAACTGTCGGGGTAAACTGGTAATATGGGCGTAAACCTGTCCGGGTAAACGGCTTTGTC
                                                                   GTAACTGTCGGG--TAAACTGTAATATGGCGTAA----CTGTCGGGTAAACGGCTTTGTC
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall;
site 2: Notl; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
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IMAGE:30285241 5', mRNA sequence
CB318729
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High quality sequence stop: 581.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Leslie L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 787)
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National Institutes of Health, Mammalian
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GGAGAGTGTAACCATTCCTTCCACAACTGCTGCATGTCCCTGTGGGTGAAACAGAACAAT
                                                                                 (ggccattatggcc); Site 2: Sfil (ggccgctggcc); 5' and 3' adaptors were used in loning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCAGGCGGCGACATGATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCGACATGATGGCC-3' and 3' adaptor sequence: 6'-ATTCTAGAGGCCGAGGCGGCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.6-3.5 kb). 15/15 colonies contained insert by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
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/lab_host="DHIOB (T1-phage-resistant)"
/lab_nost="NNH MGC_165"
/note="Organ: testis; Vector: pDNR-LIB; Si
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/db_xref="taxon:10090"
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Pred. No. 3e-133;
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BG917948.1 GI:14298424
EST.
Mus musculus (house mouse
Mus musculus
                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM10903 row: i column: 20
                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 916)
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National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
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                                                                                     quality sequence stop: 760.
Location/Qualifiers
/organism="Mus musculus"
/mol type="mRNA"
/strain="FVB/N"
/db xref="taxon:10090"
/clone="IMAGE:4949851"
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Similarity 93.8%;
61; Conservative
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                              GCAAGCGGAGGCAACCTGTTGTCTTCATTTG
                                                                                       ATAAAATGGCGTTGAAAGAGCCGAATCCTTCCTAAATCGTTGTAGTGTAGGGGAGAGAG
                                                                                                           TAAAA----TGCATTGAAAAGCCGACTCCTCCTAATCCTTTTTGTGT----TGGGAGAGAG
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/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DHIOB"
/clone_lib="NCI_CGAP_Mam6"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal_Site_2: Not1; Cloned unidirectionally. Primer: Oligo d_Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"
a 202 c 264 g 218 t
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AGENCOURT 11293247 NIH MGC 164 Mus
IMAGS:30146934 5', mRNA sequence.
CA977674.1 GI:27510328
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National Institutes of Health, Mammalian Gene
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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1 (bases 1 to 944)
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CDNA Library Arrayed by: The I.M.A.G. E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information ca
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GCCAGCAGGACTGGGTAGTCCAAAGAATCGGCAAATGAGAGGTGGCCCAGGCGCTCCTGG
                                                                                                                                                                                                                               TTCGATGTCAAGCTGAAAACAAGCAAGAGGACTGTGTTGTTGTCTGGGGAGAGAGTGTAACC
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                                                                                                                            ATTCCTTCCACAACTGCTGCATGTCCCTGTGGGTGAAACAGAACAATCGCTGCCCTCTGT
                                                                                  ATTCCTTCCACAACTGCTGCATGTCCCTGTGGGTGAAACAGAACAATCGCTGCCCTCTGT
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/clone="IMAGE:30146934"
/clone="IMAGE:30146934"
/lab_host="PHH10B (phage resistant)"
/clone_lib="NIH_MGC_164"
/clone="Vector: pCMV-SPORT6:1.ccdb; Site_1: EcoRV; Site_2:
/note="Vector: pCMV-SPORT6:1.ccdb; Site_2: EcoRV; Site_2:
/note="Vector: pCMV-SPORT6:1.ccdb; Site_2: EcoRV; Site_2: EcoRV;
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/mol_type="mRNA"
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BQ177475.1
                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BQ177475 676 bp mRNJ
UI-M-ERO-bwo-n-12-0-UI.rl NIH_BMAP_ERO
IMAGE: 5699915 5', mRNA sequence.
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National Institutes of Health,
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                 Unpublished
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/db_xref="taxon:10090"
/clone="TWAGE: 5699915"
/tissue_type="whole brain"
/dev_stage="embryo_15.5 dpc"
/lab_host="DH10B (T1 phage r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       804
                                                                                   /organism="Mus musculus"
/mol_type="mRNA"
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                                                                      strain="C57BL/6"
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ACGGTTAAAAA 671
                                   AGGGTTAAAAA 688
                                                                                                   TGTACCCACGACT---GGAACATTGTGTTTCACAGAAGAACATTGTTTTGTGTTTATGCTTG
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/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed_according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNa was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
, is GTGCGTGAA. This library was created for the
University of lowa Mouse Brain Molecular Anatomy Project
(BMAP): 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Instututes of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."
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99.4%;
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Pred. No. 1.7e-129;
0; Mismatches 1;
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Best Local Similarity
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Tissue Procurement: Dr. James Lin, Univeristy of Iowa
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 686)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BQ044727.1 GI:19795492
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UI-M-EMO-bvm-j-14-0-UI.rl NIH_BMAP_
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                                                                           GCAAATGAGAGGTGGCCCAGGCGCTCCTGGTGTGGTTGCTGACCCTGGACAAAAGACTAAA 410
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CACTGCAGGGGATTCATCCTTGAGAGAGAGAGATGCTGTGCGCCTTTGAGACTCACCAA 470
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                                                                                                                                             GGGTGAAACAGAACAATCGCTGCCCTCTGTGCCAGCAGGACTGGGTAGTCCAAAGAATCG
                                             GCAAATGAGAGGTGGCCCAGGCGCTCCTGGTGTGGTTGCTGACCCTGGACAAAGACTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="whole brain"
/dev gtage="embryo 18.5 dpc"
/lab_host=_PUH10B (T1 phage resistant)"
/clone lib="NIH BMAP EM0"
/clone lib="NIH BMAP EM0"
/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
Site 2: Not I; The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNa was size fractionated on a 1% agarose
gil. First strand cDNA synthesis was primed with an
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

135.c 174 g 197 t 1 others
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/mol_type="mRNA"
/strain="C57BL/6"
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98.7%;
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Pred. No. 4.2e-129;
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                                                                                                                             Email: cgapbs r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11149 row: m column: 17
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BI147544.1 GI:14607545
EST.
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602913971F1 NCI_CGAP_Li9
                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 754)
                                                                                                                      High
                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
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                                                                                                         quality sequence stop: 669.
Location/Qualifiers
/mol_type="mRNA"
/mol_type="mRNA"
/strain="FVB/N"
/strain="FVB/N"
/db_xref="reaxon:10090"
/clone="IMAGE:5055160"
/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NCI (GAP_Li9"
/note="Organ: līver; Vector: pCMV-SPORT6; Site_1: NotI;
                                                                                organism="Mus
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                                            BF018804 / יעי עף www.83b03.x1 McCarrey Eddy type B clone IMAGE:3655085 3' similar PROTEIN SAG. ;, mRNA sequence.
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      musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Marra M/WashU-NCI Mouse EST Project 1999
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
CTGTGTTGTGGTCTGGGGAGAGTGTAACCATTCCTTCCACAACTGCTGCATGTCCCTGTG
                                                                                                          CTTTCTTCGCACTCCGGNAGCGCAGGCTCCAAGTCGGGAGGCGACAAGATGTTCTCTCCA
                                                                                                                                                                               AGAAAGTGGACCNCGGTAGCCCATGTGGAGCTGGGACGTTGAGTGCGATACCTGTGCCAT
                                                                                                                                                                                                              AAGAAGTGGAACGCGGTAG-CCATGTGGAGCTGGGACGTTGAGTGCGATACCTGTGCCAT
                                                                             mmalia; Eutheria; (bases 1 to 704)
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314 286 1810
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//lab_host="mblob" (phage-resistant) (phage-resistant)
//lab_host="mblob" (phage-resistant) (phage-res
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Pred. No. 5.7e-129;
0; Mismatches 7;
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532 GTTAAAAATGGCCTTTCCTACCTCTGGTGTGTGTGTGTGATACGAATGCATAGAAGAGCG
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                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLAM9527 row: h column: 12
High quality sequence stop: 687.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; I (bases 1 to 946)
NIH-MGC http://mgc.nci.nih.gov/.
National_Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP_Li9"
/note="Organ: liver; Vector: pcMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                                                                                                                                                                           /organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
                                                                                                                     /db_xref="taxon:10090"
/clone="IMAGE:4194107"
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Tissue Procurement: Dr. Leslie L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished Contact: Robert Strausberg, Ph.D.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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                          /clone_lib="NCI_CGAP_Mam3"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Ōligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
                                                                                                                                                /tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="mRNA"
/strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
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Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach
                                                                                        Mus musculus (house mouse)
Mus musculus
                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., Khong H. T., Kawasawa, Y., Kedzierski, R.M., Kanara, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., Kanara, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., Kawaji, H., Kawasawa, Y., Kedzierski

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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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MRL:http://genome.gsc.riken.go.jp/
Adachi_J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda
Adachi_J., Aizawa,K., Akimura,T., Arakawa,T., Hori,F., Imotani,K.,
S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K.,
Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno
H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,
Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Re 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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                                                                                                                                                                 /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                /sex="female"
                                                                                                                    /clone="I530025D07"
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/tissue_type="placenta"
/dev_stage="14 days pregnant adult"
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                                                                                                                                                                                 AATTTGTCTGTTTAGTTTTGGGAAATTCTCTACAATTAAGATAATTTGTTAAAAATGGCC
                                                                                                              ATGATCTTTGTTTATCTGTACCCACGACTG 634
                                                                                                                                       TTTCCTACCTCTGGTGTGTGTGTGATACGAATGCATAGAAGAGCGAGAACACCAGANA
                                                                                                                                                    TTTCCTACCTCTGGTGTGTGTGTGTGTGTATACGAATGCATAGAAGAGCGAGAACACCAGAAA
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GI:28250800
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Pred. No. 2.9e-124;
0; Mismatches 1;
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REFERENCE AUTHORS TITLE JOURNAL KEYWORDS SOURCE COMMENT VERSION ORGANISM CB209237.1 EST. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 920)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Email: cgapbs-r@mail.nih Tissue Procurement: Dr. I Unpublished Mus musculus Mus musculus (house mouse) Contact: Robert Strausberg, Ph.D. David Rowe and Dr. Mina

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BASE COUNT
ORIGIN
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Matches 642
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Location/Qualifiers
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TTCACAGAAGAACATTGTTTTGTGTTTATGCTTGAGGGTTAAAAAATAGA 693
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                                                                                       AGCGAGAACACCAGAAAATGATCTTTGTTTATCTGTACCCACGACT----GGAACATTGTG
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//lab host="DH10B (phage-resistant)"
//lab host="PH10B (phage-resistant)"
//clone="lib="NIH_MGC_164"
//clone_lib="NIH_MGC_164"
//clone_lib="NIH_MGC_164"
//clone_lib="Yector: pCMV-SPORTS.1.ccdb; Site_1: EcoRV; Site_2:
//note="Vector: pCMV-SPORTS.1.cdb; Site_1: EcoRV; Site_2:
//note="Vector: pCMV-SPORTS.1.cdb; Site_1: EcoRV; Site_2:
//note="Vector: pCMV-SPORTS.1.cdb; Maxilla and mandible, day
pooled mouse embryonic limb, maxilla and mandible, day
10.5 and 11.5 (size selected for the 0.5-1 kb fragments)
Cloned directionally, priming method: Oligo-dT. cDNA
enrichment: lk bp. Average insert size 1.8k bp. Priming
sequence: 5'GACTAGTTCTAGATCGCGAGCGGCGCCC(T) 3'. Tissue
contributed by, David Rowe. Library constructed by Resden,
Invitrogen Corp."

84 a 152 c 200 g 194 t 190 others
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/db_xref="taxon:10090"
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Pred. No. 7.1e-124;
0; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                     306
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Tissue Procurement: Jeffrey E. Green, M.D.

Tissue Procurement: Jeffrey E. Green, M.D.

Tissue Procurement: Jeffrey E. Green, M.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM9455 row: a column: 09 High quality sequence stop: 738.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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National Institutes of Health, Mammalian
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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EST.
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                                                                              GGGGAGAGTGTAACCATTCCTTCCACAACTGCTGCATGTCCCTGTGGGTGAAACAGAACA
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                                                       GGGGAGAGTGTAACCATTCCTTCCACAACTGCTGCATGTCCCTGTGGGTGAAACAGAACA
                                                                                                                                                                                                                                          CGGTAGCCATGTGGAGCTGGGACGTTGAGTGCGATACCTGTGCCATCTGCAGGGTCCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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/lab host="DH108 (T1 bhage-resistant)"
/lab host="DH108 (T1 bhage-resistant)"
/clone lib="NCI (GAP SC2"
/note="Organ: sallvary gland; Vector: pCMV-SPORT6; Si NotI; Site 2: Sall; Cloned unidirectionally. Primer: dT. Average insert size 1.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
a 178 c 229 g 188 t
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/strain="FVB/N"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          xref="taxon:10090"
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Pred. No. 2.8e-123;
0; Mismatches 11;
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                                                                                                                                                                                              Email: cgapbs-romail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM9792 row: e column: 13
High quality sequence start: 3
High quality sequence start: 3
High quality sequence stop: 631.
Location/Qualifiers
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Mammalia; Eutheria; Rodentia; Sciurognath
1 (bases 1 to 755)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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602095851F1 NCI_CGAP_Co24 Mus
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/db_xref="taxon:10000"
/clone="IMAGE:4215924"
/lab host="DH10B (T1 phage-resistant)"
/lab host="DH10B (T1 phage-resistant)"
/clone lib="NCI CGAP CO24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: Sall; Cloned unidirectionally. Primer: Oligo di
Site_2: Sall; Cloned unidirectionally. Primer: Oligo di
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

167 c 218 g 188 t
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'mol_type="mRNA"
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           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 620)
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Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                               AAAATGATCTTTGTTTATCTGTACCCACGACT----GGAACATTGTGTTTCACAGAAGAACA
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                                            AAAATGATCTTTGTTTATCTGTACCCACGACTGTGGGAACATTGTGTTCACAGAAGAACA
                                                                                                         GCCTTTCCTACCTCTGGTGTGTGTGTGATACGAATGCATAGAAGAGCGAGAACACCAG
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/note="Vector: pT773D-Bac (Pharmacia) with a modified
polylinker; lst strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
and cloned into the Not I and Eco RI sites of the
modified pT773 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo. "
a 167 c 118 g 171 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
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/db_xref="taxon:10090"
/clone="IMAGE:3373340"
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98.9%;
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AUTHORS
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SOURCE
ORGANISM
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Tanaka, T.S., Jaradat, S.A., Lim, M.K., Kargul, G.J., Wang, X., Grahova, M.J., Pantano, S., Sano, Y., Piao, Y., Nagaraja, R., Doi, H., Wood, W.F. III, Becker, K.G. and Ko, M.S. H.
Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdnaelgsun.grc.nia.nih.gov Plate: L0259 row: F column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: George J. Kargul
Laboratory of Genetics
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2.56ug of total RNA. The double-stranded cDNAs were treated with T4 DNA polymerase and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal3 (include Sal1 sequence). The cDNAs were purified by phenol/chloroform and separated from free linkers by Centricon 100. Then, cDNAs were amplified by long-range high fidelity PCR using Takara's Ex Tag polymerase. Then, the cDNAs were purified by phenol/chloroform and by Centricon 100. The cDNAs were digested with Sal1 and Not1 enzymes. Then, the cDNAs were size selected by Gibco's Size Fractionation Column. The cDNAs were cloned into Sal1/Not1 site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by chemical method. The library was constructed by Xiaohong Wang and Yulan Piao."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="Newborn Ovary"
/lab_host="DH10B"
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'clone="L0259F11"
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Mouse Newborn Ovary cDNA Library Mus musculus cDNA
3', mRNA sequence.
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                              CB951114 728 bp mR AGENCOURT 13442509 NIH MGC 177 Mus mu IMAGE:30316022 5', mRNA sequence. CB951114 GI:30206005 EST. Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54
               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can
                                                                                                                                                                                       Mus musculus Eukaryota; Metazoa; Chordata; Craniata; V Eukaryota; Metazoa; Chordata; Sciurognath Mammalia; Eutheria; Rodentia; Sciurognath 1 (bases 1 to 728)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGGTGTGTGTGTGTGATACGAATGCATAGAAGAGCGAGAAACACCAGAAAATGATCTTTG
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through the I.M.A.G.E. Consortium/LLNL at:
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Pred. No. 3.4e-117;
0; Mismatches 0;
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Sciurognathi;
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thi; Muridae; Murinae; Mus
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/ Clone | 1b="NIH MGC 177"
/ Mote="Organ: liver; Vector: pDNR-LIB; Site_1: Sfil (ggccgcttcggcc); cDNA made (ggccattatggcc); Site_2: Sfil (ggccgcttcggcc); cDNA made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in cloning as follows: adaptors were used in cloning as follows: adaptors were used following as follows: adaptors were used following as follows: a part of the clone of the contain contain the con
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K.,
Ishi,Y., Itoh,M., Kagawa,I., Kawai,J., Kojina,Y., Kondo,S., Konno,H., Kaya,S., Miyazaki,A., Murata,M., Namura,K.,
Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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EST.
Mus musculus (house mouse)
                                                                                                                                                    Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 171-1630 (2018) system--384-format REEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Re 10 (11), 1757-1771 (2000)
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                                 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construencedundant cDNA library. Genome Res. 11 (2), 281-289
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Contact: Yoshihide Hayashizaki
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library was prepared and sequenced in Mouse Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp)
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                  GCTTTGAGTTATATAAGTTTGATATATATACTCTTAAAATCATTAAACTAATTCATC 1131
                                                                                          GAAAATGGCTTACTAGTATAACACTGAAGTTCATTATGCAATGTTTTAATAAAAATATTGT
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                                                                                                                                        GAACTGTTTTCTGTTTTTG-CGAAGGTTGTATTGTATGTTTTAGTC-AAAATATTAGTAG
                                                                                                                                                          TGACTTCTCCATCTTTGACTTGGCCAGGAAGCCTGGATTGTTCAACCACTTAGTTCTAAA
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                                                                    GAAAAT-GCTTACTAGTATAACACTGAAGTTCATTATGCAATGTTTTAATAAAATATTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="placenta"
/dev_stage="14 days pregnant adult"
/clone_lib="RIKEN full-length enriched, 14 days
adult female placenta"
103 c 135 g 223 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTGTTTATGCTTGAGGGTTAAAAAATAGATAAACGAATGTTACAGTAACAAA
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Best Local Similarity
Matches 606; Conserv
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Tissue Procurement: Dr. James Lin, Univeristy of Iowa
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/Libra at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 624)
NIH-MGC http://mgv.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BM946344.1 GI:19429929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone was contributed by the
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                                                                                                                                                                                              GACGITGAGIGCGATACCIGIGCCAICIGGCAGGGTCCAGGIGAIGGAIGCCIGCCIICGA 205
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                                                                                                                                                                                                                                                                                                                                                                            TCGGGAGGCGACAAGATGTTCTCTCTCAAGAAGTGGAACGCGGTAGCCATGTGGAGCTGG 145
                                              TGTCAAGCTGAAAACAAGCAAGAGGACTGTGTTGTGGTCTGGGGAGAGTGTAACCATTCC
                                                                                                                                                   TGTCAAGCTGAAAACAAGCAAGAGGACTGTGTTGTGGTCTGGGGAGAGTGTAACCATTCC
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/dev_stage="embryo 18.5 dpc"
/lab_host="PulOB (TI phage resistant)"
/clone_lib="NIH_BMAP_EMO"
/clone_lib="NIH_BMAP_EMO"
/clone_lib="NIH_BMAP_EMO"
/clone_lib="NIH_BMAP_EMO"
/clone_lib="NIH_BMAP_EMO"
/clone_lib="NIH_BMAP_EMO"
/clone_lib="NIH_BMAP_EMO"
/clone_lib="NIH_BMAP_EMO"
/clone_lib="NIH_BMAP_EMO"
/clone_morgan: brain; Vector: pyx-Asc; Site_l: EcoR I;
/note="Gorgan: brain; Vector: pyx-Asc; Site_l: EcoR I;
/note="Gorgan: brain; Vector: pyx-Asc; Site_lib-"29.806,
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
Bonaldo, Leonome Research,
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Pred. No. 1.3e-114;
0; Mismatches 1;
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266 TTCCACAACTGCTGCATGTCCCTGTGGGTGAAACAGAACAATCGCTGCCCTCTGTGCCAG
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 757)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Leslie L.
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National Institutes of Health, Mammalian
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/tissue_type="primary cultures of Sertoli cells"
/lab host="phi0B (T1-phage-resistant)"
/clome lib="NH10B (T1-phage-resistant)"
/clome lib="NH1 MGC 165"
/clome lib="NH1 MGC 165"
/note="Organ: testis; Vector: pDNR-LIB; Site_1: SfiI
/ggccattatggcc); Site_2: SfiI (ggccgctcggcc); 5' and 3'
adaptors were used in_cloning as follows: 5' adaptor
adaptors were used in_cloning as follows: 5' adaptor sequence:
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
s'-ATTCTAGAGGCCGAGCGGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4 kb
(range 0.6-3.5 kb). 15/15 colonies contained inserts by
                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/mol_type="mRNA"
/db xref="taxon:10090"
/clone="IMAGE:30283955"
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                                                     N AGENCOURT 14123281 NIH MGC 176 Mus mu
IMAGB:30380219 5', mRNA sequence.
CD241479
CD241479.1 GI:31001943
EST.
Mus musculus (house mouse)
M Mus musculus
Eukaryota; Metazoa; Chordata; Craniat
Mammalia; Eutheria; Rodentia; Sciurog
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Unpublished Contact: Robert Strausberg, Email: cgapbs-r@mail.nih.gov
                                NIH-MGC http://mgc.nci.nih.gov/.
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156 c 206 g 192 t 1 others
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             GGCCTTT-CCTACCTCTGGTGTGTGTGTGTGATACGAATGCATAGAAGAGCGAGAACA--
                                                          TATTAATTTGTCTGTTTTAGTTTTTGGGAAATTCTCTACAATTAAGATAATTTGTTAAAAAT
                                                                                                         GGTGGCCCAGGCGCTCCTGGTGTGGTGCTGACCCTGGACAAAGACTAAACACTGCAGGG
                                                                                                                                                                                                      GAACAATCGCTGCCCTCTGTGCCAGCAGGACTGGGTAGTCCAAAGAATCGGCAAATGAGA
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GGCCTTTCCCTACCTCCGGTGTGTGTGTGTGTGATACCAATGCATTGAAGAGCGAGAACACC
                                                                                                                                           GGTGGCCCAGGCGCTCCTGGTGTGGTTGCTGACCCTGGACAAAGACTAAACACTGCAGGG
                                                                                                                                                                                         GAACAATCGCTGCCCTCTGTGCCAGCAGGACTGGGTAGTCCAAAGAATCGGCAAATGAGA
                                                                                                                                                                                                                                         GGTCTGGGGAGAGTGTAACCATTCCTTCCACAACTGCTGCATGTCCCTGTGGGTGAAACA
                                                                                                                                                                                                                                                                                        GAACGCGGTAGCCATGTGGAGCTGGGACGTTGAGTGCGATACCTGTGCCATCTGCAGGGT
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Location/Qualifiers
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Pred. No. 7.5e-114;
0; Mismatches 16;
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Indels Length

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180 123

120 63

603

543 540

597

480

483

423 420 363 360 303 300

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Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information ca
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Dlate: NDCM171 row: o column: 12
/mol_type="mRNA"

/db_xref="taxon:1090"

/clone="IMAGE:30380219"

/lab host="DHIOB (T1-phage-resistant)"

/lab host="DHIOB (T1-phage-resistant)"

/clone_lib="NIH_MGC_176"

/note="Organ: kidney; Vector: pDNR-LIB; Site_1: Sfil

(ggccattatggcc); Site_2: Sfil (ggccgcctcggcc); cDNA made

by oligo-dT priming and directionally cloned. 5' and 3'
adaptors were used in cloning as follows:
5'-AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGG-3' and
5'-ATTCTAGAGCCGGACAGTGGCCATTACGGCCGGG-3' and
5'-ATTCTAGAGCCGGCCGACATTG-dT(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.5 kb
size fraction. Library created in the laboratory of M.
Brownstein (NIMH, NIH). Note: this is a NIH_MGC Library."
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Best Local Similarity
Matches 575; Conserv
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BF023423
BF023423.1 GI:10754756
                             121
                                                       148
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to 575)

1 (Chaes 1 to 575)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.J.
Contact: Robert Strausberg, Ph.J.
Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@mailable royalty-free through LLNL; contact the This clone is available royalty-free through TLNL; contact the This clone is available royalty-free through TLNL; contact the This clone is available.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus
                                                                                                            88
                                                                                                                                                           28 GGAGGACGGCGAGGAACCCTGCGTCCTTTCTTCGCACTCCGGGAGCGCAGGCTCCAAGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMAGE Consortium (info@image.llnl.gov)
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                                                                                                     GGGAGGCGACAAGATGTTCTCTCTCAAGAAGTGGAACGCGGTAGCCATGTGGAGCTGGGA 147
                           GGGAGGCGACAAGATGTTCTCTCAAGAAGTGGAACGCGGTAGCCATGTGGAGCTGGGA
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Thymus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sex="male"
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CB600846
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: Dr. Michael Brownstein

CDNA Library Preparation: Michael Brownstein Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can
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AGENCOURT 13037376 NIH MGC 176 Mus
IMAGE:30313065 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CB600846.1 GI:29518702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://image.llnl.gov
Plate: NDCM99 row: a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 462.
Location/Qualifiers
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by oligo-dT priming and directionally cloned. 5' and 3'
adaptors were used in cloning as follows:
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adaptors were used in cloning as follows:
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 735)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
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602870803F1 NCI_CGAP_Mam2
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                                                         Unpublished
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                       CTATCTGTACCCACGACTGTGGGACACATTGTGCTCACAGAAGA
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/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone="IMAGE:5002729"
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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAMM1038 row: e column: 02
High quality sequence stop: 622.
Location/Qualifiers
                                                                                                                                                                       can
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/tissue_type="tumor, biopsy sample"
/dev stage="5 months"
/lab_host="DH10B"
/clone lib="NCI_CGAP Mam2"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Ōligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
a 185 c 201 g 176 t

Score 568.8; DB 12; Pred. No. 2:3e-111; 0; Mismatches 12; Indels Length 8 4

CCATTCCTTCCACAACTGCTGCATGTCCCTGTGGGTGAAACAGAACAATCGCTGCCCTCT CCATTCCTTCCACAACTGCTGCATGTCCCTGTGGGTGAAACAGAACAATCGCTGCCCTCT 300 318

GTGCCAGCAGGACTGGGTAGTCCAAAGAATCGGCAAATGAGAGGTGGCCCAGGCGCTCCT

378

360

GGTGTGGTTGCTGACCCTGGACAAAGACTAAACACTGCAGGGGATTCATCCTTGACGAGA GGTGTGGTTGCTGACCCTGGACAAAGACTAAACACTGCAGGGGATTCATCCTTGA--GAG

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568 bp mRNA linear EST 03-JAN-2001 mab59f05.yl Soares thymus 2NbMT Mus musculus cDNA clone IMAGE:9974553 5' sīmilar to TR:Q9WTZ1 Q9WTZ1 ZINC RING FINGER PROTEIN SAG. ;, mRNA sequence.

BF720947

BF720947
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Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 568)
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National Cancer Institute, Cancer Genome Anat
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TCCCTGTGGGTGAAACAGAACAATCGCTGCCCTCTGTGCCAGCAGGACTGGGTAGTCCAA
                                                                                            138
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Soares thymus_2NbMT"
/clone_lib="Soares thymus_2NbMT"
/note="Wector: pT7\pideliber]

polylinker; Site 1: Not I; Site_2: Eco RI; 1st strand cDNA
polylinker; Site 1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I oligo(dT) primer [5'

was primed with a Not I of the Site RI adaptors
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/clone="IMAGE:3974553"
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pred. No. 5.6e-111;
0; Mismatches 1;
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Marra M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA230335.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                         Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
Fax: 314 286 1810
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCACCAAAGGCTTGCTTTATTAATTTGTCTGTTTTAGTTTTGGGAAATTCTCTACAATTAA 523
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the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. " 142 a 124 c 164 g 147 t
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Search completed: November 7, 2003, 15:15:38 Job time : 2889.08 secs

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Maximum DB seq length: 2000000000
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Perfect score:
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
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Result No.	Score	Query	Query Match Length	DB	ID .	Description
<u></u>	124	100.0	342	ا و	US-09-826-312-7	Sequence 7, Appli
2	124	100.0	342	14	US-10-108-767-7	Sequence 7, Appl:
ω	124	100.0	342	14	US-10-152-156-7	7
4.	124	100.0	612	10	US-09-796-692-8547	854
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œ	95	76.6	535	14	US-10-102-524-396	396,
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13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	14.5	14.5	1
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US-09-764-891-6245	US-10-133-013-222	US-09-925-297-338	US-10-084-817-86	US-10-044-090-218	US-09-981-353-121	US-10-133-013-221	US-10-281-904-1	US-10-264-374-200	US-10-205-823-31	US-09-880-107-2295	US-10-281-904-3	US-10-027-632-255720	US-10-027-632-255720	US-10-027-632-162983	US-10-027-632-162982	US-10-027-632-162983	US-10-027-632-162982	US-10-027-632-145248	US-10-027-632-145248	US-09-918-995-31855	US-10-066-543-1656	US-09-864-761-21703	US-09-864-761-4974	US-10-027-632-276727	US-10-027-632-276727	US-10-106-698-799	US-10-027-632-31061	
6245,	Sequence 222, App	Sequence 338, App			Sequence 121, App	Sequence 221, App					Sequence 3, Appli	Sequence 255720,	Sequence 255720,			Sequence 162983,				Sequence 31855, A	•	Sequence 21703, A	4974,	Sequence 276727,			Sequence 31061, A	

ALIGNMENTS

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; SEQ ID NO 7
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-312-7
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US-09-826-312-7
; Sequence 7, Application US/09826312
; Patent No. US20020042083A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                        Query Match 100.0%; Score 124; DB 9; Best Local Similarity 100.0%; Pred. No. 6.9e-60; Matches 124; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: UBIQUITIN LIGASE ASSAY FILE REFERENCE: A-68613-1/RMS/JJD CURRENT APPLICATION NUMBER: US/09/826,312 CURRENT FILING DATE: 2001-04-03 PRIOR APPLICATION NUMBER: US 09/542,497 PRIOR FILING DATE: 2000-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Issakani, Sarkiz D. APPLICANT: Huang, Jianing APPLICANT: Sheung, Julie APPLICANT: Pray, Todd R.
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                                     121 CTGC 124
                                                                          201
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                                                                                                1 CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGGCTGTCTTAGATGTCAAGCTGA 60
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; ORGANISM: Homo sapiens
US-10-108-767-7
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Publication No. US20030104474A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/10152156
Publication No. US20030108947A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 124; Conservative
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FILE REFERENCE: A-68613-5/RMS/DCF
CURRENT APPLICATION NUMBER: US/10/108,767
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 09/542,497
PRIOR FILING DATE: 2000-04-03
PRIOR FILING DATE: 2000-04-03
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 09/826,312
PRIOR APPLICATION NUMBER: US 09/826,312
PRIOR APPLICATION NUMBER: US 10/091,139
                                                                                                                                                                                                                                                                               TITLE OF INVENTION: ASSAYS FOR IDENTIFYING UBIQUITIN AGENTS AND FOR IDENTIFYING AGENTITLE OF INVENTION: MODIFY THE ACTIVITY OF UBIQUITIN AGENTS FILE REFERENCE: A-68613-6/RMS/DCF
                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/152,156
CURRENT FILING DATE: 2002-05-20
                                                                                                                                                 PRIOR APPLICATION NUMBER: US 09/826,312 PRIOR FILING DATE: 2001-04-03
                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 09/542,497 PRIOR FILING DATE: 2000-04-03
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Issakani, Sarkiz D. APPLICANT: Huang, Jianing
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NUMBER OF SEQ ID NOS: 27
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                                                                                                          APPLICATION NUMBER: US 10/091,174 FILING DATE: 2002-03-04
                                                             APPLICATION NUMBER: US 10/091,139 FILING DATE: 2002-03-04
                      APPLICATION NUMBER: US 10/109,460 FILING DATE: 2002-03-26
APPLICATION NUMBER: US 10/108,767
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Pray, Todd R.
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Pred. No. 6.9e-60;
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RESULT 4
US-09-796-692-8547
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                                                                                                                                                                PRIOR FILING DATE: 2000-05-22

PRIOR APPLICATION NUMBER: 60/218,950

PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: 60/222,903

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: 60/223,416

PRIOR APPLICATION NUMBER: 60/223,416

PRIOR APPLICATION NUMBER: 60/223,378

PRIOR APPLICATION NUMBER: 60/223,378

PRIOR FILING DATE: 2000-08-07
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CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR PELICATION NUMBER: 60/190,479
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
                                                                                   SEQ ID NO 8547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8547, Application US/09796692 Publication No. US20020198362A1
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NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.1
                                                                                                                     SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/202,084
                                                                                                                                               NUMBER OF SEQ ID NOS: 9597
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PRIOR APPLICATION NUMBER: 60/206,201
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ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
                                  TYPE: DNA
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                                                            ENGTH: 612
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Pred. No. 6.9e-60;
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FEATURE: NAME/KEY: unsure LOCATION: (485)

OTHER INFORMATION: n=A,T,C or

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RESULT 5
US-10-040-862-8547
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 Query Match
                                                                                                                                         SEQ ID NO 8547
LENGTH: 612
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Best Local Similarity
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TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
CURRENT APPLICATION NUMBER: US/10/040,862
CURRENT FILING DATE: 2001-11-06
                                                                                                                                                                      NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR
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PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
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                                            OTHER INFORMATION: n=A,T,C or
                                                          NAME/KEY: unsure
LOCATION: (485)
                                                                                             FEATURE:
                                                                                                          ORGANISM: Homo sapiens
                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                 FILING DATE: 2000-05-22
APPLICATION NUMBER: US 60/218,950
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APPLICATION NUMBER: US 60/222,903
FILING DATE: 2000-08-03
APPLICATION NUMBER: US 60/223,416
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Mannion, Jane
Retter, Marc
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 100.0%;
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 Score 124;
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; TYPE: DNA; ORGANISM: Homo sapiens US-09-764-864-39
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US-09-764-864-39
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APPLICANT: Rosen et al.
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrappe
NUMBER OF SEQ ID NOS: 1792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 39
LENGTH: 836
                                                                                                             SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 498
                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
                                                                                                                                                                                                                                                                           Sequence 498, Application US/09764864
Patent No. US20020132753A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                             CURRENT FILING DATE: 2001-01-17
Prior application data removed -
NUMBER OF SEQ ID NOS: 1792
                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
               ORGANISM: HOMO S
FEATURE:
NAME/KEY: SITE
LOCATION: (45)
OTHER INFORMATION: n equals a,t,g,
                                                                              TYPE: DNA
                                                                                                 ENGTH: 836
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                                                               sapiens
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Pred. No. 6.9e-60;
); Mismatches 0;
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                                                                                                                                                                consult PALM or file wrapper
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APPLICANT: Gordon, Brian
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF KIDNEY CAI
FILE REFERENCE: 210121,572
CURRENT APPLICATION NUMBER: US/10/102,524
CURRENT FILING DATE: 2002-03-19
NUMBER OF SEQ ID NOS: 1863
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 396
LENGTH: 535
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US-10-198-846-12407
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; NAME/KBY: misc feature
; LOCATION: 14, 24, 32, 206, 240, 361, 384, 439,
; OTHER INFORMATION: n = A,T,C or G
US-10-102-524-396
             GENERAL INFORMATION:

APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS,
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
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US-10-102-524-396
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                                                                                                                                                       Sequence 12407, Application US/10198846 Publication No. US20030099974A1
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Best Local
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Publication No. US20030109434A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Algate, Paul A.
APPLICANT: Mamnion, Jane
APPLICANT: Gaiger, Alexander
APPLICANT: Gordon, Brian
CURRENT APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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NUMBER: US/10/198,846
                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                           76.6%;
                                                                                                                                                                                                                                                                                                                                                                                        Score 95; DB 14; Length 535; Pred. No. 1.7e-43;
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Pred. No. 6.9e-60;
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                                         AND METHODS PREVENTION,
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RESULT 11 US-10-198-846-7306

Sequence 7306, Application US/10198846 Publication No. US20030099974A1

GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzher

APPLICANT:

Xu, Yongyao Wang, Youzhen Steinmann, Kathleen

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                                                                                                                                    ; ORGANISM: Homo sapiens US-09-908-975-13285
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US-09-908-975-13285
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; LOCATION: 1, 2, 1022, 1023, 1
; OTHER INFORMATION: n = A,T,C
US-10-198-846-12407
                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 13285
                                                                    Matches
                                                                                                  Query Match
                                                                                                                                                                                                                                      APPLICANT: SHOSHAN, Avi
APPLICANT: WASSERWAN, Alon
APPLICANT: WASSERWAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: MINTZ, Liat
APPLICANT: MINTZ, Liat
APPLICANT: FAIGLER, Simchon
TITLE OF INVENTION: OLICONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-07-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13285, Application US/09908975
Publication No. US20030165843A1
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PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                TYPE: DNA
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ORGANISM: Homo sapiens
FEATURE:
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                                                                  Local Similarity nes 35; Conserv
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CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGG
                      CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGG 35
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                                                                  Conservative
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C or G
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                                                                               Score 35; DB 12;
Pred. No. 1.3e-0
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                                                               Mismatches
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0;
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60
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RESULT 12
US-09-974-026-61/c
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                                                           CURRENT FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 09/144,428
PRIOR APPLICATION NUMBER: US 09/144,428
PRIOR APPLICATION NUMBER: PCT/US97/03894
PRIOR APPLICATION NUMBER: US 08/725,251
PRIOR APPLICATION NUMBER: US 08/725,251
PRIOR FILING DATE: 1996-10-04
PRIOR PILING DATE: 1996-10-04
PRIOR APPLICATION NUMBER: US 60/019,793
PRIOR APPLICATION NUMBER: US 60/013,106
PRIOR APPLICATION NUMBER: US 60/013,106
PRIOR FILING DATE: 1996-06-14
PRIOR FILING DATE: 1996-06-3-11
SOFTWARE:
SEQ ID NO (
LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 61, Applica Publication No. US20 GENERAL INFORMATION:
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Best Local 9
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SEQ ID NO 7306
LENGTH: 933
                                                PRIOR FILING DATE: 1996-0
NUMBER OF SEQ ID NOS: 105
                                                                                                                                                                                                                                       FILE REFERENCE: 96-223-ZZ
CURRENT APPLICATION NUMBER: US/09/974,026
CURRENT FILING DATE: 2001-10-10
                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Tamburini, Paul P
APPLICANT: Davis, Gary
                                                                                                                                                                                                                                                                                         APPLICANT: Delaria, Katherine A
APPLICANT: Christopher, Marlor W
APPLICANT: Daniel, Wuller K
TITLE OF INVENTION: Human Bikunin
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LOCATION: 672, 674, 680,
LOCATION: 725, 733, 740,
LOCATION: 769, 771, 774,
LOCATION: 769, 801, 802,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS TITLE OF INVENTION; FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND TITLE OF INVENTION: THERAPY OF BREAST CANCER FILE REFERENCE: MRI-049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 819, 824, 827,
LOCATION: 876, 882, 893,
LOCATION: 919, 925, 927,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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OTHER INFORMATION: n
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LOCATION: 36, 150, 168,
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NO 61
TH: 45
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INFORMATION: n = A,T,C or G
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No. US20030194398A1
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Pred. No.
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904,
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747,
783,
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748,
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762,
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915,
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Sequence 113318, Application US/10027632

Publication No. US20030204075A9

GENERAL INFORMATION:
APPLICANT: Wang, David G.

ITILE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE REFERENCE: 108627.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILLING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILLING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILLING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILLING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/185,363

PRIOR FILLING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILLING DATE: 1999-09-28

PRIOR FILLING DATE: 1999-09-28
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US-10-027-632-113318/c
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: POlymorphisms in the Human Genome
TITLE OF INVENTION: POLYMORER: US/10/027,632
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
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Best Local
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Best Local :
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100.0%; Pred. No.
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US-09-998-598-450/c
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; OTHER INFORMATION: n = A,T,C or
US-09-918-995-19059
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; Sequence 19059, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
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                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                   Sequence 450, Application US/09998598 Patent No. US20020150922A1
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Matches
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Best Local Similarity
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SEQ ID NO 113318
LENGTH: 3372
                                APPLICANT: Xu, Jiangchun
APPLICANT: Chenault, Ruth A.
APPLICANT: Meagher, Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FO
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.561
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                                                                                        APPLICANT: Stolk, John A. APPLICANT: Xu, Jiangchun APPLICANT: Chenault, Rut APPLICANT: Meagher, Made
CURRENT APPLICATION NUMBER: US/09/998,598
CURRENT FILING DATE: 2001-11-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
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CURRENT FILING DATE: 2001-07-30
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PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
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PRIOR FILING DATE: 1999-09-28
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NAME/KEY: misc_feature
'-' '226'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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19; Conserv
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100.0%; Pr/
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                                                                     AND METHODS FOR THE THERAPY AND
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RESULT 18
US-10-027-632-31061
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US-10-027-632-31061
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PRIOR FILLING DATE: 2000-02-24
PRIOR PELLORITION NUMBER: US 60/167,363
PRIOR FILLING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILLING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                     Sequence 31061, Application US/10027632 GENERAL INFORMATION:
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Best Local Similarity
Matches 18; Conser
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SOFTWARE: FastSEQ for Windows
SEQ ID NO 31061
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
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SOFTWARE: Corixa Invention Disclosure Database
SEQ ID NO 450
LENGTH: 541
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Best Local
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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CURRENT FILING DATE: 2002-04-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Human
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Local Similarity 100.0%;
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Pred. No.
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RESULT 20
US-10-027-632-276727/c
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, NAME/KBY: misc feature
; LOCATION: (1676)..(1676)
; OTHER INFORMATION: n equals a,t,g, or
US-10-106-698-799
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US-10-106-698-799/c
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Sequence 276727, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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SEQ ID NO 799
LENGTH: 2630
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31061
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Best Local Similarity
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Best Local (
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CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
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PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03
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TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
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FILING DATE: 1999-11-23
APPLICATION NUMBER: US 60/156,358
FILING DATE: 1999-09-28
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SOFTWARE: FastSEQ for
SEQ ID NO 276727
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SEQ ID NO 276727
LENGTH: 252
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
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PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-11-23
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PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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                                        Local Similarity
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18 GCAGGGTCCAGGTGATG 34
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                                        Conservative
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100.0%; Pr
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                                                           Score 17; Pred. No.
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Pred. No.
                                        Mismatches
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19;
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GCAGGGTCCAGGTGATG 35

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US-09-864-761-4974
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US-09-864-761-4974
Query Match
Best Local Similarity
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SEQ ID NO 4974
LENGTH: 355
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CURRENT FILING DATE: 2001-05-23
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PRIOR FILING DATE: 2000-02-04
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ORGANISM: Homo
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APPLICATION NUMBER: PCT/US01/00664
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Score 17;
Pred. No.
                                                                                                                                                               FETAL LIVER, SIGNAL = 1.6
BRAIN, SIGNAL = 1.1
LUNG, SIGNAL = 1.3
HEART, SIGNAL = 1.7
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PLACENTA, SIGNAL =
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                                                                                                          HELA, SIGNAL = 1.3
ADULT LIVER, SIGNAL =
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RESULT 23
US-09-864-761-21703
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PRIOR APPLICATION NUMBER: PCT//
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT//
PRIOR TILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 61
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PRIOR FILING DATE: 2000-09-21
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SEQ ID NO 21703
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
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PRIOR TELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
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PRIOR FILING DATE: 2000-09-27
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CURRENT FILING DATE: 2001-05-23
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FILING DATE: 2001-01-30
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Hanzel, David K.
Chen, Wensheng
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EXPRESSED IN BT474, 6 
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D IN HBL100, SIGNAL = 1.5
D IN PLACENTA, SIGNAL = 2
D IN FETAL LIVER, SIGNAL = 1
D IN BRAIN, SIGNAL = 1.1
D IN LING, SIGNAL = 1.3
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APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBT
TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILLING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 31855
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US-10-066-543-1656
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CURRENT APPLICATION NUMBER: US/10/066,543
CURRENT FILING DATE: 2007-01-31
NUMBER OF SEQ ID NOS: 3417
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1656
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Best Local S
Matches 17
                                                                                                                                                                     Sequence 31855, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1656, ... Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Jiang, rugen
APPLICANT: Dvle, Ruth A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 211, 453, 454
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
OTHER INFORMATION: NT HIT: AB019786.1, EVALUE 1.20e-02
OTHER INFORMATION: EST_HUMAN HIT: AA495851.1, EVALUE 2.20e-01
OB-66.751.751.7170.
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                                                                                                                                                                                                                                                                                                              433 CCATCTGCAGGGTCCAG 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281 GGTCCÁGGTGÁTGGÁTG 297
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                                                                                                                                                                                                                                                                                                                                   CCATCTGCAGGGTCCAG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Secrist, Heather
Carter, Darrick
Fanger, Gary R.
Smith, Carole L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Durham, Margarita
Stolk, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indirias, Carol
Lodes, Michael J
                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/10066543 US20030087818A1
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Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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19;
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RESULT 27
US-10-027-632-145248/c
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US-09-918-995-31855
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PRILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-02-4
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
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LENGTH: 712
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Matches
                                                                                                                                                                     Sequence 145248, Application US/10027632 GENERAL INFORMATION:
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.1.29
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1999-09-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(500)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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100.0%; Pred. No.
Live 0; Mismatc
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; LENGTH: 833
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-162982
RESULT 29
US-10-027-632-162983
; Sequence 162983, Application US/10027632
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US-10-027-632-162982
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; ORGANISM: Human
US-10-027-632-145248
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Best Local Similarity
                                                                                                                                                                                               Matches
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SEQ ID NO 145248
LENGTH: 712
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Publication No. US20030204075A9
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Best Local Similarity
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0 EQ ID NO 162982
                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 325720
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR OTTING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
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FILING DATE: 2000-02-24
APPLICATION NUMBER: US 60/167,363
FILING DATE: 1999-11-23
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                                                                                                             TGTCAAGCTGAAAACAA 210
                                                                                                                                     TGTCAAGCTGAAAACAA 66
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100.0%; Pred. No.
cive 0; Mismatc
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19;
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19;
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; LENGTH: 833
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-162983
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                                                              ; ORGANISM: Human US-10-027-632-162982
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US-10-027-632-162982
                                                                                                                                                      SEQ ID NO 162982
                       Query Match
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, David G.
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                    PRIOR FILING DATE:
                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/156,358 PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/167,363 PRIOR FILING DATE: 1999-11-23
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                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/185,218 PRIOR FILING DATE: 2000-02-24
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PRIOR APPLICATION NUMBER: US 60/193,483
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CURRENT FILING DATE: 2002-04-30
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                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-03-29
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PRIOR APPLICATION NUMBER: US 60/185,218
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PRIOR FILING DATE: 2000-04-20
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                                                                                                                            LENGTH: 833
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APPLICATION NUMBER: US 60/156,358
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Pred. No.
Score 17;
Pred: No.
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DB 13;
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RESULT 32
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-02-24
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
FILE REFERENCE: 108827.129
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
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PRIOR APPLICATION NUMBER: US 60/193,483
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ORGANISM: Human
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                                                                                   APPLICATION NUMBER: US 60/167,363 FILING DATE: 1999-11-23
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                                                                APPLICATION NUMBER: US 60/156,358
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PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
                                                                                                                    Sequence 3, Application US/10281904
Publication No. US20030119036A1
GENERAL INFORMATION:
APPLICANT: Chun, Miyoung
TITLE OF INVENTION: METHODS OF USING 48149,
TITLE OF INVENTION: AMINOPEPTIDASE FAMILY N
FILE REFERENCE: MP101-174P1RM
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Best Local Similarity
Matches 17; Conserv
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SOFTWARE: FastSEQ for
SEQ ID NO 255720
LENGTH: 1781
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CURRENT APPLICATION NUMBER: US/10/281,904
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 60/335,084
PRIOR FILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 1999-08-09
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CURRENT FILING DATE: 2002-04-30
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LENGTH: 2904
TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                      Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 2295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2295, Application US/09880107
Patent No. US20020142981A1
                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                          APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E
APPLICANT: Endege, Wilson
                                                     TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, K
TITLE OF INVENTION: METHODS FOR IDENTIFICATION,
THERAPY OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
               CURRENT FILING DATE:
                                                                                                     APPLICANT:
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NUMBER OF SEQ ID NOS: 3950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/211,379 PRIOR FILING DATE: 2000-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/237,054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Horne,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 3494
REFERENCE: MRI-044
REFERENCE: MRI-044
ENT APPLICATION NUMBER: US/10/205,823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vockley, Joseph G
Scherf, Uwe
Gene Logic, Inc.
                                                                                                                          Hoersch, Sebastian
Kamatkar, Shubhangi
Wonsey, Angela M.
                                                                                                   Anderson, Dustin
                                                                                                                                                                                              Gannavarapu, Manjula
Gorbatcheva, Bella
                                                                                                                                                                                                                          Monahan, John E.
Endege, Wilson O.
                                                                                                                                                                                                                                                                                   Application US/10205823 to. US20030108963A1
                                                                                                                     Zhao, Xumei
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                          John E
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; Pred. No.
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; Pred. No. 19;
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                                                                     ASSESSMENT, PREVENTION,
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RESULT 38
US-10-281-904-1/c
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; LOCATION: (121)..(3024)
US-10-264-374-200
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CURRENT APPLICATION NUMBER: US/10/264,374

CURRENT FILING DATE: 2002-10-03

PRIOR APPLICATION NUMBER: US/09/139,802

PRIOR FILING DATE: 1998-08-25

PRIOR APPLICATION NUMBER: 08/926,914

PRIOR FILING DATE: 1997-09-10

PRIOR APPLICATION NUMBER: 08/710,067

PRIOR FILING DATE: 1996-09-10
                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Pate
SEQ ID NO 200
LENGTH: 3494
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                                                                                                                                                     Query Match
Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
TITLE OF INVENTION: Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/362,158
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR FILING DATE: 2001-12-12
                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ruoslahti, Erkki
APPLICANT: Pasqualini, Ren
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/307,982
                                                                                                                                                                                                                                                                                            FEATURE
                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 17; Conserv
                                                                            1762 CCATCTGCAGGGTCCAG 1746
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                                                                                                                CCATCTGCAGGGTCCAG
                                                                                                                                                         Conservative
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100.0%; Pred. No.
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                                                                                                                                                                         DB 14;
. 19;
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Sequence 1, Application US/10281904
Publication No. US20030119036A1
GENERAL INFORMATION:

APPLICANT: Chun, Miyoung
TITLE OF INVENTION: METHODS OF USING 48149, A HUMAN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FEATURE:
; NAME/KBY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030166903A1 1136923.19
US-10-133-013-221
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                                                                                  GENERAL INFORMATION:
APPLICANT: Lasek, Amy W.
APPLICANT: Jones, David A.
APPLICANT: Jones, David A.
TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
FILE REFERENCE: PA-0038 US
CURRENT APPLICATION UNMER: US/09/981,353
CURRENT FILING DATE: 2001-10-11
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                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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SEQ ID NO 221
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CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 60/335,084
PRIOR FILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FRESESEQ for Windows Version 4.0
SEQ ID NO 1
             NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL Program
SEQ ID NO 121
LENGTH: 3686
                                                                                                                                                                                                                 Sequence 121, Application US/09981353 Patent No. US20020160382A1
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Astromoff, Anna
APPLICANT: Bandman, Olga
APPLICANT: Cocks, Benjamin G.
TITLE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE
FILE REFERENCE: PA-0049 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/133,013
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: 60/287,067
PRIOR FILING DATE: 2001-04-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 3494
TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH: 3681
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; Pred. No.
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TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION FILE REFERENCE: PA-0046 US CURRENT APPLICATION NUMBER: US/10/084,817 CURRENT FILING DATE: 2002-02-25 PRIOR APPLICATION NUMBER: 60/270,784 PRIOR APPLICATION NUMBER: 60/270,784 PRIOR FILING DATE: 2001-02-23 NUMBER OF SEQ ID NOS: 365 SOFTWARE: PERL PROGram SEQ ID NO 86 LENGTH: 3686
                                                ; TYPE: DNA; ORGANISM: Homo sapiens; FEATURE:
; PEATURE: misc feature; NAME/KEY: misc feature; OTHER INFORMATION: Incyte ID No. US20030119009A1 1344279CB1 US-10-084-817-86
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; OTHER INFORMATION: Incyte ID No. US20020160382A1 1344279CB1
US-09-981-353-121
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US-10-044-090-218/c
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SEQ ID NO 218
LENGTH: 3686
TYPE: DNA
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                    Publication No.
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APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Susan Stuart
APPLICANT: Jed G. Nuchtern
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NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20020137081A1 1344279CB1
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No. US20030119009A1
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 13.7%;
100.0%;
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100.0%; Pred. No.
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 DB 14;
19;
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; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incy
US-10-133-013-222
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US-10-133-013-222/c
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/287,067
PRIOR FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 271
SOFTWARE: PERL Program
SEQ ID NO 222
LENGTH: 3815
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         Matches
                                             Query Match
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Publication No. US20030166903A1
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SEQ ID NO 338
LENGTH: 3728
                                                                                                                                                                                                                                                                                                 APPLICANT: Astromoff, Anna
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Cocks, Benjamin G.
TITLE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE
FILE REFERENCE: PA-0049 US
CURRENT APPLICATION NUMBER: US/10/133,013
CURRENT FILLING DATE: 2002_04-25
DEFICE APPLICATION TOWNS TO THE APPLICATION NUMBER: US/10/133,013
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Patent No. US20020081659A1
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 928
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OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
LOCATION: (3713)
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                           Local
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   l Similarity 100.
17; Conservative
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                                                                                             Incyte ID No.
 13.7%; Score 17; DB 12;
100.0%; Pred. No. 19;
tive 0; Mismatches 0
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100.0%; Pred. No.
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               ; ORGANISM: Homo sapiens US-10-205-428-561
                                                SOFTWARE: Paten
SEQ ID NO 561
LENGTH: 11150
TYPE: DNA
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Sequence 6245, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
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GENERAL INFORMATION
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6245
LENGTH: 11150
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PRIOR APPLICATION NUMBER: 60/218,290
PRIOR FILING DATE: 2000-07-14
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CURRENT FILLING DATE: 2002-07-26
PRIOR APPLICATION NUMBER: 09/764,892
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
                                                                                                                           Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 1019
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/180,628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PA117C1
                                                                                                                                                                                                                 RIOR APPLICATION NUMBER: 60/225,447
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                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/217,496 FILING DATE: 2000-07-11
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; ORGANISM: Homo Sapiens
US-09-682-706-1
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APPLICANT: Hsueh, Aaron
APPLICANT: Hsueh, Aaron
TITLE OF INVENTION: Stresscopins and their ses
FILE REFERENCE: STAN210
CURRENT APPLICATION NUMBER: US/09/682,706
CURRENT FILLING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/276,615
PRIOR FILLING DATE: 2001-03-15
PRIOR FILLING DATE: 2000-10-26
PRIOR FILLING DATE: 2000-10-26
NUMBER OF SEO ID NOS: 15
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SEQ ID NO 8350
LENGTH: 253
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701101059H1
                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09682706
Patent No. US20020082409A1
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Best Local Similarity
                                                                    Matches
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Patent No. US20020110548A1
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Best Local :
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (15401) B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
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                                                                                                                                                                                     ENGTH: 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115
                                83
                                                                16;
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                              GTGGTCTGGGGAGAAT 98
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                                                                  Conservative
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100.0%; Pred. No.
tive 0; Mismatc
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NUMBER OF SEQ ID NOS: 5912
SEQ ID NO 5910
LENGTH: 397
TYPE: DNA
ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-919-473-1/c
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APPLICANT: Warren, W.
APPLICANT: Tao, Nene
APPLICANT: Byatt, J.
APPLICANT: Mathialae
                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 13
SEQ ID NO 1
1.ENCOMO
                                                                              Query Match
Best Local :
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                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 37-21(10297)C
CURRENT APPLICATION NUMBER: US/09/983,965
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: US 09/465,231
PRIOR FILING DATE: 1999-12-15
                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/919,473
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/273,969
PRIOR FILING DATE: 2001-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Vale, Wylie Walker Jr. APPLICANT: Lewis, Kathy Ann
                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                       LOCATION: 7..345
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 7..
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PPLICANT: Rivier, Jean Edouard Frederic
PPLICANT: Perrin, Marilyn Heller
PPLICANT: Proteins and Uses Thereof
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                                                                                                                                                                                                                                                                                        ENGTH: 399
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                      83
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16; Conser
GTGGTCTGGGGAGAAT 98
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Reyes, Teresa Marie
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Sawchenko, Paul Emil
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                                                          12.9%; Score 16; larity 100.0%; Pred. No. Conservative 0; Mismatc
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                                                                                                                                                       DNA Sequence encoding human 
Urocortin-related peptide (
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                                                          ore 16; DB 10;
Pred. No. 70;
Mismatches 0
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122 GTGGTCTGGGGAGAAT 107

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Search completed: November 7, 2003, 13:55:40 Job time : 479.215 secs

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Result
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Perfect score:
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Maximum DB
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1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*

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Copyright (c) 1993 - 2003 Compugen Ltd
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                            AAA96883
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13.7	13.7		14.5	14.5	14.5	14.5	٠	٠	15.3	19.4	19.4	19.4	25.8	28.2	28.2	33.1	33.9	34.7	59.7	59.7	61.3	66.9	71.8	72.6	٠	•	•		86.3			97.6	100.0	100.0	100.0	100.0
355	355	239	2630	2405	2405	541	349	18	45	630	596	264	1140	439	60	441	706	224	754	754	754	754	1152	747	754	754	754	754	754	754	754	754	962	836	836	836
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ABA51431	ABA46329	AAS84630	AAH33733	AAQ92962	AAQ70827	ABV87139	AAC29980	AAX87337	AAA70390	AAL22239	AAL25052	AAL16209	AAX87313	ABZ11414	ABN40537	AAC77493	AAX87316	AAX41085	AAX87329	AAX87327	AAX87328	AAX87320	AAH25847	AAX87315	AAX87321	AAX87326	AAX87322	AAX87319	AAX87318	AAX87323	AAX87317	AAX87324	AAC77504	ABX73660	ABX73201	AAS26319
breast		DNA encoding novel	Human colon cancer	Human HRR25-like c	Protein kinase (CK			Human sensitive to	directed			Human breast cance		Human polynucleotí		ORFX ORF3	Human sensitive to	secreted pr	sensitive	sensitive	sensitive t	sensitive	apoptosis a	sensitive	_	Human ORFX ORF3059		nove]	Human cDNA encodin							

RESULT 1 AAA96883 ID AAA9 XX AAA9 AC AAA9 XX Nucl XX ROC1 KW ROC1 KW Cull KW WO21 KW WO21 KW WO21 KW WO21 Homo sapiens. ROC1; ROC2; cullin; ring finger protein; APC11; APC complex; SCF pathway; cullin dependent ubiquitin ligase; CDK inhibitor Sic1 degradation; Nucleotide sequence of human ring finger protein ROC2 19-FEB-2001 AAA96883; AAA96883 standard; DNA; 342 BP (first entry) /*tag= a /product= "ROC2" /transl except= (Location/Qualifiers

ALIGNMENTS

05-OCT-2000.

WO200058472-A2

: sod) : sod) : sod) : sod) : sod)

28.30, aa: Pro)
34.36, aa: Val)
40.42, aa: Sel)
58.60, aa: Ala)
67.69, aa: Lys)
109.111, aa: Ala

aa: Ala

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RESULT 2
AAH43570
ID AAH4
XX AAH4
AC AAH4
XX AAH4
XX AAH4
XX AAH4
XX WASSA
KW ASSA
KW Ubiq
XX Ubiq
XX Unid
XX Unid
XX WO20
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XX WO3-A
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Best Local :
                                                                                                                                                        Assay; ubiquitin ligase; tag1-ubiquitin; E1; E2; ubiquitin activating enzyme; ubiquitin conjugating enzyme; E3; ubiquitin ligase; ubiquitination modulator; ss.
                    03-APR-2000; 2000US-0542497
                                                   03-APR-2001; 2001WO-US10906
                                                                                                        WO200175145-A2
                                                                                                                                   Unidentified
                                                                                                                                                                                                               ROC2 coding
                                                                                                                                                                                                                                         07-JAN-2002
                                                                                                                                                                                                                                                                                            AAH43570 standard; cDNA; 342 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes a human ROC2 ring finger protein. The specification also describes human ROC1. ROC1 and ROC2 are similar to APC11, a subunit of the APC complex. The proteins stimulate cullin dependent ubiquitin ligase activity. ROC1 functions in vivo as an essential regulator of CDK inhibitor Sic1 degradation by the SCF (undefined) pathway. ROC proteins are useful for screening bioactive agents that interfere with the binding of ROC proteins with cullin proteins. Pharmaceutical formulations comprising ROC proteins are useful for diagnostic and therapeutic purposes, preferably for
  (RIGE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 342 BP; 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosing and treating tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acid encoding termed as ROC proteins simil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-1999;
22-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 18; Fig 2B; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               therapeutic and diagnostic use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAB19161.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYNC-) UNIV NORTH CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-2000; 2000WO-US08592
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 RIGEL PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
                                                                                                                                                                                                                                                                                                                                                                                        CTGC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
                                                                                                                                                                                                                                                                                                                                                               CTGC 264
                                                                                                                                                                                                                                                                                                                                                                                                                Ohta T;
                                                                                                                                                                                                               sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid encoding cullin regulating ring finger proteins, proteins similar to anaphase-promoting complex 11, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0127261.
99US-0166927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; 84 C; 108 G; 68 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 124; DB 2
Pred. No. 1e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
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RESULT 3
AAD39674
ID AAD3
XX AAD3
AC AAD3
XX AAD3
XX AAD3
XX Ubiq
CH Huma
XX Ubiq
KW E2;
KW E2;
KW RING
XX RING
XX Homo
XX KHOMO
XX HOMO
XX HOMO
XX HOMO
XX HOMO
XX HOMO
XX KEY
FT CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cubiquitin conjugating enzyme) and E3 (ubiquitin ligase) and measuring the amount of tag1-ubiquitin bound to the E3. The method is useful for assaying ubiquitin ligase activity and ubiquitination enzyme activity condition is useful for identifying ubiquitination modulator. The method comprises combining tag1-ubiquitin, the modulator, E1 E2 and tag2-E3 cand measuring the amount of tag1-ubiquitin bound to tag3-E2 or combining c2 tag1-ubiquitin modulator, E1 and tag3-E2 and measuring the amount of c3-E2. Ubiquitin ligase activity is measured c3 cdirectly, eliminating the need from unligated measuring the amount of c3-E3. Ubiquitin ligated activity is measured c3 cdirectly, eliminating the need from unligated material in an c5 chalysis such as separating ligated from unligated material in an c5 chroughput screening techniques for modulators of ubiquitination c2 combinations of E3 components and E2/E3 combinations without requiring c1 prior identification of specific target substrates. Ubiquitin is labeled, c3 cdirectly or indirectly and this allows for easy and rapid detection and c3 cmeasurement of ligated ubicmitin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 124;
                                                                                                     Ubiquitin ligase; UL; tag1-ubiquitin; E1; ubiquitin-activating enzyme; E2; ubiquitin-conjugating enzyme/ubiquitin carrier protein; E3; human; RING finger protein; gene; ds.
                                                                                                                                                                              Human RING finger protein,
                                                                                                                                                                                                                     22-OCT-2002
                                                                                                                                                                                                                                                         AAD39674;
                                                                                                                                                                                                                                                                                          AAD39674 standard; DNA; 342 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequences given in AAH43568-72 encode proteins which may be used in the method of the invention for assaying ubiquitin ligase activity. The method comprises combining under conditions that favour ubiquitin ligase activity, tag1-ubiquitin, E1 (ubiquitin activating enzyme), E2 (ubiquitin conjugating enzyme) and E3 (ubiquitin ligase) and measuring the amount of tag1-ubiquitin bound to the E3. The method is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 200
P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   measurement of ligated ubiquitin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           conjugating enzyme,
bound to the ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assaying ubiquitin ligase activity for identifying modulators of ubiquitination, by combining ubiquitin, ubiquitin activating conjugating enzyme, ubiquitin ligase and measuring amount of ubiquitin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Fig 12A; 98pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Issakani
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGC 264
                                                                                                                                                                                                                                                                                                                                                                                                                     CTGC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                342 BP; 82 A; 84 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                ROC2 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 124; DB 2
Pred. No. 1e-55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22;
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Homo

sapiens

Location/Qualifiers
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RASSULT 4
AAXA8732
ID AAXX
XX AAXX
XX AAXX
XX AAXX
DT 27-5
CX SAG
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an assay for ubiquitin ligase (UL) activity which comprises incubating tag1-ubiquitin, El (ubiquitin-activating enzyme), E2 (ubiquitin-conjugating enzyme/ubiquitin carrier protein) and E3 (UL) and measuring the amount of tag1-ubiquitin bound to E3. The method is particularly used to screen for modulators of UL activity. The present sequence is human RING finger protein, ROC2 DNA.
                                                                                                                                                                                                           SAG gene; sensitive to apoptosis; human; cancer; tumour; neurodegenerative disease; muscular dystrophy; wound healing; vulnerary; therapy; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assay for ubiquitin ligase activity, useful for identifying modulators, by measuring binding of labeled ubiquitin to ubiquitin ligase
     WO9932514-A2
                                                                         mutation
                                                                                                                                                            Synthetic.
                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                Human sensitive to
                                                                                                                                                                                                                                                                                                                    27-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                    AAX87325 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 12A; 56pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-APR-2000; 2000US-0542497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              342 BP; 82 A; 84 C; 108 G; 68 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
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                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             264
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                                                      replace(295,T)
/*tag= b
                                                                                                                          Location/Qualifiers
                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product= "Human ROC2 protein"
                                                                                                                                                                                                                                                                                                                                                                                      CDNA;
                                                                                                                                                                                                                                                                                apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                     "C99S mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sheung
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 124; DB 24; Pred. No. 1e-55;
                                                                                                                                                                                                                                                                                (SAG) gene mutant MM9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ٦
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 342;
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                                                                                                                                                                                                                         RESULT 5
AAX87330
ID AAX8
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Best Local &
Homo sapiens
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         141
                                                                                                                                                                                                                                                                                                                  261
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Matches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oligomerization. These properties were unaffected by the MM9 mutation. SAG is a novel zinc finger protein that promotes cell growth, protects cells from apoptosis, scavenges oxygen radicals and can be used for the reversion of a tumour phenotype. SAG genes, and mutant SAG genes, can be used to protect cells from apoptosis induced by redox reagents. They can also be used for the recombinant production of SAG proteins, which are molecular targets in the development of drugs against neurodegenerative disorders, cancers and muscle dystrophy, and promoting wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is the nucleotide sequence of human sensitive to apoptosis (SAG) mutant gene MM9, which codes for a SAG protein (see AAY06503) in which the Cys residue at position 99 of the native protein (see AAY06492) is replaced by a Ser residue owing to a mutation of codon 99 from TGC to AGC obtained by site-directed mutagenesis of SAG CDNA. This residue is in zinc-ring finger 2 of SAG. Single and double SAG mutants (see AAX87317-31) were made in order to determine the role of each cysteine residue of SAG in hem binding and SAG
                      SAG gene; sensitive to apoptosis; neurodegenerative disease; muscula
                                                                                              Human sensitive
                                                                                                                                                                                                                                           AAX87330 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAG: Sensitive to Apoptosis Gene and related proteins, useful promoting cell growth and protecting cells against apoptosis
vulnerary;
                                                                                                                                               27-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-430152/36
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19-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Page 72-73; 84pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                            CTGC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 206 A; 155 C; 201 G; 192 T; 0 other;
                                                                                                                                             (first
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97US-0068179.
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                                                                                              to apoptosis
                                                                                                                                                                                                                                           CDNA; 754
    mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                        muscular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                              (SAG)
                                                                                                                                                                                                                                           Β₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 124;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                               human;
                                                                                              gene mutant MM14.
                        dystrophy; wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1e-55;
                                               cancer; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
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Location/Qualifiers

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RESULT 6
AAX87331
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                                                                                                                                                                         В
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                                                                                                                                                                                                                                                                                                                                 This is the nucleotide sequence of human sensitive to apoptosis (SAG) mutant gene MM14, which codes for a SAG protein (see AAY06508) in which the Cys residues at positions 99 and 102 of the native protein (see AAY06492) are replaced by Ser residues owing to mutations of codons 99 and 102 through site-directed mutagenesis of SAG cDNA. These residues are in zinc ring finger 2 of SAG. Single double SAG mutants (see AAX87317-31) were made in order to determine the role of each cysteine residue of SAG in haem binding and SAG oligomerization was observed, indicating that these residues are important for intermolecular disulfide bond formation. SAG is a novel zinc finger protein that promotes cell growth, protects can be used to protect cells from apoptosis, scavenges oxygen radicals and can be used for the reversion of a tumour phenotype. SAG genes, and mutant SAG genes, can be used to protect cells from apoptosis induced by redox reagents. They can also be used for the recombinant production of SAG proteins, which are molecular targets in the development of the strength beginning the service of the strength beginning the service and muscle strength of the service and success and muscle strength.
                                                                                                                                                                                                                                     Matches 124;
                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9932514-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAG: Sensitive to Apoptosis Gene and related proteins, useful promoting cell growth and protecting cells against apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-SEP-1998;
19-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1998;
                                                                                                                                                                                                                                                                                           Sequence 754 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 15; Page 81; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAY06508.
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                                                                                                                 201
                                                                                                                                                                           141
                                                                                    121
                                                          261
                                                                                                                                              61
                                                                                                                                                                                                          _
                                                                                                                                   CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
                                                                                                                                                                           CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
                                                                                       CTGC 124
                                                                                                                 and promoting wound healing.
                                                                                                                                                                                                                                    Conservative
                                                          264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0099840.
97US-0068179.
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/*tag= b
/note= "C998 mutation"
replace(304,C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "C102S mutation"
                                                                                                                                                                                                                                                                                            207
                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                           A; 155 C;
                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                    Score 124; DB 20;
Pred. No. 1e-55;
; Mismatches 0;
                                                                                                                                                                                                                                                                                            201 G; 191 T; 0 other;
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                    754;
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                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                              200
                                                                                                                     260
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19

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                                                                     Query Match
Best Local S
                                                        Matches 124;
                                                                                                                                            oligomerization. These properties were unaffected by the MM15 mutation. SAG is a novel zinc finger protein that promotes cell growth, protects cells from apoptosis, scavenges oxygen radicals and can be used for the reversion of a tumour phenotype. SAG genes, and mutant SAG genes, can be used to protect cells from apoptosis induced by redox reagents. They can also be used for the recombinant production of SAG proteins, which are molecular targets in the development of drugs against neurodegenerative disorders, cancers and muscle dystrophy, and promoting wound healing.
                                                                                                                                                                                                                                                                             This is the nucleotide sequence of human sensitive to apoptosis (SAG) mutant gene MMIS, which codes for a SAG protein (see AAY0650; in which the Cys residue at position 47 of the native protein (see AAY06492) is replaced by a Ser residue owing to a mutation of codor 47 from TGC to AGC obtained by site-directed mutagenesis of SAG CDNA. This residue is in a GADPH binding, site of SAG. Single and double SAG mutants (see AAX87317-31) were made to determine to the of each cysteine residue of SAG in haem binding and SAG comparation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sun
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAG: Sensitive to Apoptosis Gene and promoting cell growth and protecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAG gene; sensitive to apoptosis; human; cancer; tumour; neurodegenerative disease; muscular dystrophy; wound hea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-SEP-1998;
19-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vulnerary; therapy; mutant;
                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 15; Page 82-83; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-430152/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (WARN ) WARNER LAMBERT CO
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                                                                          Local Similarity
                                                                                                                   754 BP; 206 A; 155 C; 201 G; 192 T; 0 other;
CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
                            CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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97US-0068179.
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/*tag= b
/note= "C47S mutation"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  apoptosis (SAG)
                                                                        100.0%;
                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          muscular dystrophy; wound healing; ds.
                                                          o
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                                                                        Score 124; DB 2
Pred. No. 1e-55;
                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                    related proteins, useful cells against apoptosis
                                                                                      20;
                                                           0;
                                                                                      Length
                                                                                           754;
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RESULT 7
AAX87314
ID AAX8
AX AAX8
AX AAX8
AX SAG
AX
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                                                                                                             This is the nucleotide sequence of human sensitive to apoptosis (SAG) cDNA, which codes for a novel redox sensitive, haem-binding protein (see AAY06492) with a zinc RING finger domain that promotes cell growth, protects cells from apoptosis, scavenges oxygen radicals and can be used for the reversion of a tumour phenotype. The cDNA was isolated from a HeLa cell cDNA library using mouse SAG cDNA (see AAX87313) as probe. SAG is highly conserved among species. Disruption in yeast was shown to be lethal. SAG deletion mutants (see AAX87315-16) have been identified in human cancer lines, suggesting a role in carcinogenesis. SAG genes, and mutant SAG genes, can be used to protect cells from apoptosis induced by redox reagents. Antisense SAG genes can be used to inhibit the growth of the sAG genes can also be used for the recombinant production of the SAG genes can also be used for the recombinant concerns the same of the sAG proteins. The SAG proteins can be used to promote or inhibit the growth of plant cells (all claimed). The SAG protein is also an ideal molecular target in the development of during against neurodegenerative disorders, cancers and muscle
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAG: Sensitive to Apoptosis Gene and related proteins, useful promoting cell growth and protecting cells against apoptosis
                                                             Sequence 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-430152/36 P-PSDB; AAY06492.
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19-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human sensitive to apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX87314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (WARN ) WARNER LAMBERT CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9932514-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vulnerary; therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAG gene; sensitive to apoptosis; human; cancer; tumour; neurodegenerative disease; muscular dystrophy; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Page 50-51;
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                                                             BP;
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97US-0068179.
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1..342
100.0%;
                                                        A; 155 C; 201 G; 193 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP
Score 124; DB 20;
Pred. No. 1e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                Length 754;
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AAS25860
ID AAS2
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14-AUG-
14-AUG-
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
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07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
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16-MAR-2000;
17-MAR-2000;
18-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nervous system disorder; Alzheimer's disease; infection; ocu corneal infection; wound healing; epithelial cell proliferat skin ageing; food additive; preservative; antiproliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiovascular disorder; cardiovascular disorder; cereborovascular disorder; cereboral ischaemia; anglogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disor corneal infection; wound healing; epithelial cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootro neuroprotective; antibacterial; virucide; fungicide; opthal
                                                                                                                                                                                                                                                                                                                                                                                19-MAY-2000;
                                                                                                                                                                                                                                                                                                                                         30-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
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                                                         2000US-0225214.
2000US-0225266.
2000US-0225267.
2000US-0225268.
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2000US-0224518.
2000US-0224519.
2000US-0225213.
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2000US-0215135.
2000US-0216647.
2000US-0216880.
2000US-0217487.
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2000US-0209467.
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opthalmalogical;
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2000US-0249207
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Rosen CA, Barash SC, Ruben SM

WPI; 2001-488783/53. P-PSDB; AAU15873.

New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives or preservatives and

Claim 1; SEQ ID No 39; 980pp; English.

The invention relates to isolated nucleic acid molecules and their CC encoded secreted proteins. The nucleic acids and proteins are used to CC prevent, treat or ameliorate a medical condition in e.g. humans, mice, CC rabbits, goats, horses, cats, dogs, chickens or sheep. They CC are also used in diagnosing a pathological condition or susceptibility CC to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked CC immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders (e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. CC Alzheimer's disease, infections caused by bacteria, viruses and fungii CC and ocular disorders e.g. corneal infection, and many other CC disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to CC transplantation, for supporting cell culture of primary tissues, to CC expabilities, fat content, lipid, protein, carbohydrate, vitamins, capabilities, fat content, lipid, protein, carbohydrate, vitamins, capabilities, fat content, lipid, protein, carbohydrate, vitamins, capabilities, fat content, lipid, protein, carbohydrate, vitamins minerals, cofactors and other nutritional components. The present encodes a novel secreted protein components. of the inve invention.

FESUL PASSUL PAS	Be Ma
AAS26319 standard; CDNA; 836 BP. AAS26319; O7-NOV-2001 (first entry) Human CDNA encoding a novel secreted protein, Seq ID 438. Human; immunosuppressive, antiarthritic, ss, antirhaumatic, cytostatic cardiant, vesocropic; cerebropotective; nortopic, neuropotective; antibacterial, viguride, indicate; pothalmalogical; pulpraproliferative disorder; cardiant that the protein correct correct in disorder; cardiant protein; cardiart protein; pervous system disorder; cardiart protein; pervous system disorder; cardiavescular disorder; cardiart proliferation; skin ageing; food additive; preservative; antiproliferation; skin ageing; food additive; preservative, antiproliferation; Homo, sapiens. W0200155322-A2. 02-AUG-2001, 2000US-0186454, 12-MAR 2000, 2000US-0186550, 14-MAR 2000, 2000US-018650, 14-MAR 2	Best Local Similarity 100.0%; Pred. No. 1e-55; Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 1 CGATACGTGCGCATCTGCAGGGTCCAGGTGATGCCTGTCTTAGATGTCAAGCTGA 60; 1
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CA, Barash SC, SM;

2001-488783/53.

diagnosing, preventing, treating or ameused as food additives or preservatives New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and

Claim ۲. SEQ ID No 498; 980pp; English.

CC encoded secreted proteins. The nucleic acids and proteins are used to compressed to react, treat or ameliorate a medical condition in e.g. humans, mice, crabbits, goats, horses, cats, dogs, chickens or sheep. They can also used in diagnosing a pathological condition or susceptibility care also used in diagnosing a pathological condition or susceptibility compared to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in care diagnostic immunoassays e.g. radioimmunoassays or enzyme linked include autoimmune diseases e.g. replasms of the breast or liver, compared to the disorders e.g. cardiac arrest, cerebrovascular disorders e.g. corneal infection, and many other compared to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used cas a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, contents encodes a novel secreted protein of the invention. minerals, cu-monce encodes The invention relates to isolated nucleic acid molecules and their

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Best Local Similarity
Matches 124; Conserv
14-AUG-2000;
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22-AUG-2000;
30-AUG-2000;
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                                                                                                                                                                                                                                                  The invention relates to human novel polypeptides and their associated C polynucleotides. The polypeptides and polynucleotides are useful in gene CC therapy for treating, inhibiting or preventing neural disorders, immune CC system disorders (e.g. systemic lupus erythematosus, rheumatoid C arthritis and multiple sclerosis), muscular disorders, respiratory CC diseases (e.g. nasal vestibulitis, nasal polyps and sinusitis), CC reproductive disorders, gastrointestinal disorders, pulmonary disorders, CC cardiovascular disorders (e.g. congenital heart defects, Ebstein's CC anomaly and hypoplastic left heart syndrome), renal disorders (e.g. acute kidney failure and end-stage renal disease), hypoproliferative disorders (e.g. Hodgkin's disease and leukaemia), inflammatory diseases (e.g. CC (e.g. Hodgkin's disease and appendicitis), allergic reactions and CC conditions (e.g. asthma), blood related disorders (e.g. thrombosis, conditions (e.g. asthma) and cancerous diseases. CC sequences ABX73173-ABX74167 represent human novel polynucleotides of the
                                                                                                                                                             Query Match
Best Local S
Matches 124
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29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
02-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or renal disorders -
                                                                                                                                                                                                                    Sequence 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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(RUBE/)
(BARA/)
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DB; ABU54941.
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RUBEN S M
BARASH S
                                                                                                                                                                             Similarity
                                                                                                                     CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
                                                                CIGC
                                                   CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
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2000US-236367P

2000US-236369P

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2000US-237037P

2000US-237038P

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Pred.
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                                                                                                                                                             Mismatches
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No. 1e-55;
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                                                                                                                                                             Indels
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Gaps

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RESULT 11
  14-AUG-2000;
22-AUG-2000;
30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
05-SEP-2000;
21-SEP-2000;
21-SEP-2000;
22-SEP-2000;
25-SEP-2000;
25-SE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-2000
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2000US-229345P

2000US-229509P

2000US-229513P

2000US-231413P

2000US-234273P

2000US-234279P

2000US-234279P

2000US-236367P

2000US-236367P

2000US-236368P

2000US-236369P

2000US-236369P

2000US-236379P

2000US-236379P

2000US-237039P

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2000US-244617P
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2000US-22547P
2000US-22547P
2000US-225757P
2000US-225758P
2000US-22668P
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2000US-229343P
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; 2000US-224519P.
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2000US-220964P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 124;
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Best Local :
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08-DEC-2000; 2
08-DEC-2000; 2
                            immunostimulant; thrombolytic; coagulant; vasotropic; antidiabeti hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
                                                                                                                                                  vulnerary; antipsoriatic; antiparkinsonian; anticonvulsant; osteopathic; antiarthritic;
                                                                                                                                                                                                                                                                                                             Human ORFX ORF3059 polynucleotide sequence SEQ ID NO:6117.
                                                                                                                                                                                                                                                                                                                                                                                                       08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC77504 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. masal vestibulitis, masal polyps and sinustis), reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left heart syndrome), renal disorders (e.g. cute kidney failure and end-stage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and leukaemia), inflammatory diseases (e.g. septic shock, bursitis and appendicitis), allergic reactions and conditions (e.g. asthma), blood related disorders (e.g. thrombosis, atherosclerosis and myocardial infarction) and cancerous diseases.
        antianaemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 836 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to human novel polypeptides and their associated polynucleotides. The polypeptides and polynucleotides are useful in gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
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BARASH S
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                                                                                                                                                                                                                                    reading
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                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA; 962 BP
                                                                                                                                                                                                                                    frame; ORFX; detection;
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Pred. No. 1e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    221
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al; antirheumatic; antithyroid proliferative disorder; hyper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G; 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T; 1 other;
                                                                                                                                              immunosuppressant;
                                                                                                                                                                                                                                    cytostatic; hepatotropic;
                                                                                                                                                                                           nootropic; neuroprotective;
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                                                                                                              antidiabetic;
hypertension;
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192

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CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA 60

CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA

251

61

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which represent the human ORFX open reading frames 1 to 3161. The ORFX CC sequences have activities such as: cytostatic; hepatotropic; vulnerary; CC antipacviatic; antiparkinsonian; nootropic; neuroprotective; CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant; CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; CC antidiabetic; apportantion; The sequences can be used for determining the presence of or predisposition to, or preventing or treating the presence of or predisposition to, or preventing or treating CC pathological conditions associated with an ORFX-associated disorder. The mucleic acids can be used to express ORFX proteins in gene therapy concises. The proteins and nucleic acids may be used to treat cancers, CC proliferative disorders, neurodegenerative disorders, osteoarthritis, CC staff vs host disease, cardiovascular disease, diabetes mellitus, typertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, allegic and present anticon autoimune disorders, aschma, collesterial autoimune disorders, aschma, allegic allegic and present autoimune disorders, aschma, allegic allegic and present autoimune disorders, aschma, allegic allegic and present autoimune disorders.
  Query Match
Best Local S
Matches 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthm allergy; applastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive; ss.
                                                                                                                    allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and peptides derived from open reading frame useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC74446 to AAC77606 encode the proteins given in AAB40237 which represent the human ORFX open reading frames 1 to 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shimkets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000; 2000WO-US08621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CURA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000-602362/57.
    124;
                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURAGEN CORP.
                                                                                    962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 5300; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RA,
                                                                                    ВP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0540763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0127607
99US-0127636
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                                                                                  265 A; 204 C; 243 G; 250 T; 0 other;
                     100.0%;
  0;
                       Pred.
                                         Score 124;
      Mismatches
                       No.
                       1e-55;
                                         DB 21;
    0,
                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to AAB43397,
61. The ORFX
  o
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Gaps
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RESULT 13 AAX87324

AAX87324 standard; cDNA; 754

ВP

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S
                                                                                                      (SAG) mutant gene MMB, which codes for a SAG protein (see AAY06502)

(In which the Cys residue at position 88 of the native protein (see AAY06492) is replaced by a Ser residue owing to a mutation of codon 88 from TGC to AGC obtained by site-directed mutagenesis of SAG cDNA. This residue is in zinc-ring finger 2 of SAG. Single and double SAG mutants (see AAX87317-31) were made in order to determine the role of each cysteine residue of SAG in haem binding and SAG oligomerization. These properties were unaffected by the MMB mutation. SAG is a novel zinc finger protein that promotes cell growth, protects cells from apoptosis, scavenges oxygen radicals and can be used for the reversion of a tumour phenotype. SAG genes, and mutant SAG genes, can be used to protect cells from apoptosis induced by redox reagents. They can also be used for the recombinant production of SAG proteins, which are molecular targets in the development of drugs against neurodegenerative disorders, cancers and muscle dystrophy, and promoting wound healing.
                                               Matches
                                                            Query Match
Best Local
                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                   SAG: Sensitive to Apoptosis Gene and promoting cell growth and protecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-SEP-1998;
19-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                            This is the nucleotide sequence of human
                                                                                                                                                                                                                                                                                                                                                                                         Claim 15; Page 71; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAY06502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurodegenerative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAG gene; sensitive to apoptosis; human; cancer; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (WARN ) WARNER LAMBERT CO
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                                              121;
1 CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
                                                           Similarity
                                                                                                    754 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       therapy; mutant;
                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0099840.
97US-0068179.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          replace(262,T)
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                   206 A; 155 C; 201 G; 192 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "C88S mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 apoptosis
                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      muscular dystrophy; wound healing;
                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ds
                                            Score 121; DB 20;
Pred. No. 3.9e-54;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SAG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                  related proteins, useful
                                                                                                                                                                                                                                                                                                                                                                                                                  cells against apoptosis
                                                                                                                                                                                                                                                                                                                                                            sensitive to apoptosis
                                              0
                                                                     Length
                                            Indels
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                                           Gaps
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RESULT 14
AAX87317
ID AAX87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
This is the nucleotide sequence of human sensitive to apoptosis (SAG) mutant gene MM1, which codes for a SAG protein (see AAY06495) in which the Cys residue at position 50 of the native protein (see AAY06492) is replaced by a Ser residue owing to a mutation of codon 50 from TGC to AGC obtained by site-directed mutagenesis of SAG CDNA. This residue is at a haem binding site of SAG. Single and double SAG mutants (see AAX87317-31) were made in order to determine the role of each cysteine residue of SAG in haem binding and SAG oligomerization. MM1 showed reduced haem binding but unaffected oligomerization. SAG is a novel zinc finger protein that promotes cell growth, protects cells from apoptosis, scavenges oxygen radicals and can be used for the reversion of a tumour phenotype. SAG genes, and mutant SAG genes, can be used to protect cells from apoptosis induced by redox reagents. They can also be used for the recombinant production of SAG proteins, which are molecular targets in the development of drugs against neurodegenerative disorders, cancers and muscle dystrophy, and promoting wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                   Sun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                        SAG: Sensitive to Apoptosis Gene and related proteins, useful for promoting cell growth and protecting cells against apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAY06495
                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-430152/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-SEP-1998;
19-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAG gene; sensitive to apoptosis; human; cancer; tumour; neurodegenerative disease; muscular dystrophy; wound hea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX87317;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vulnerary;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 (WARN ) WARNER LAMBERT CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 ÁAACAAÁCAAGAGGACTGTGTTGTTGTTGGGGGGAGAATGTAATCATTCCTTTCCÁCAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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97US-0068179.
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/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to apoptosis (SAG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "C50S mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mutant; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene mutant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  healing;
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RESULT 15
AAX87323
ID AAX87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                   This is the nucleotide sequence of human sensitive to apoptosis (SAG) mutant gene MM7, which codes for a SAG protein (see AAY06501) in which the His residue at position 85 of the native protein (see AAY06492) is replaced by a Lys residue owing to a mutation of codon 85 from CAC to AAG obtained by site-directed mutagenesis of SAG cDNA. This residue is in zinc-ring finger 2 of SAG. Single and double SAG mutants (see AAX87317-31) were made in order to determine the role of each cysteine residue of SAG in haem binding and SAG oligomerization. These properties were unaffected by the MM7 mutation. SAG is a novel zinc finger protein that promotes
                                                                                                                                          Claim 15;
                                                                                                                                                               browotrud
                                                                                                                                                                                                                                 gun
                                                                                                                                                                                               P-PSDB; AAY06501.
                                                                                                                                                                                                                                                                        11-SEP-1998;
19-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                             mutation
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                                                                                                                                                                                                                                                                                                         15-DEC-1998;
                                                                                                                                                                                                                                                                                                                              01-JUL-1999
                                                                                                                                                                                                                                                                                                                                                    WO9932514-A2
                                                                                                                                                                                                                                                                                                                                                                                                                             Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAG gene; sensitive neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vulnerary; therapy; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human sensitive to apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-SEP-1999
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                                                                                                                                                                                                                                                    (WARN ) WARNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
            growth,
                                                                                                                                                            Sensitive to Apoptosis Gene and related proteins, useful sting cell growth and protecting cells against apoptosis
                                                                                                                                                                                                          1999-430152/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
  wth, protects cells from apoptosis, so and can be used for the reversion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGAGGACTGTTGTTGTTGGTGGGGAGAATGTAATCATTCCTTTCCACAACTGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sensitive to apurnerative disease;
                                                                                                                                         Page 69-70; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                    LAMBERT CO
                                                                                                                                                                                                                                                                        98US-0099840.
97US-0068179.
                                                                                                                                                                                                                                                                                                         98WO-US26705
                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
replace(253..255,CAC)
                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       /note= "H85K mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to apoptosis; human; cancer; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           muscular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 116; DB; Pred. No. 1.7
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SAG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G; 192 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dystrophy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.7e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 20;
scavenges oxygen
of a tumour phenotype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                          for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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RESULT 16
AAX87318
ID AAX87
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Best Local Similarity
Matches 112; Conserv
                                                                                                                                                                     Sun
                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAG genes, and mutant SAG genes, can be used to protect cells from apoptosis induced by redox reagents. They can also be used for the recombinant production of SAG proteins, which are molecular targets in the development of drugs against neurodegenerative disorders, cancers and muscle dystrophy, and promoting wound healing.
                                                                                                    SAG: Sensitive to Apoptosis Gene and promoting cell growth and protecting
                                                                                                                                    WPI; 1999-430152/36.
P-PSDB; AAY06496.
                                                                                                                                                                                                              11-SEP-1998;
19-DEC-1997;
                                                                                                                                                                                                                                                                 01-JUL-1999.
                                                                                                                                                                                                                                                                                                                                                                                                               SAG gene; sensitive to apoptosis; human; cancer; tumour; neurodegenerative disease; muscular dystrophy; wound healing; vulnerary; therapy; mutant; ds.
                                                                                Claim 15; Page 60-61; 84pp; English.
                                                                                                                                                                                                                                             15-DEC-1998;
                                                                                                                                                                                                                                                                                       WO9932514-A2
                                                                                                                                                                                                                                                                                                                                mutation
                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human sensitive to apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX87318;
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                                                                                                                                                                                         (WARN)
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                                                                                                                                                                                          WARNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAACAAACAAGAGGACTGTGTTGTGGTCTGGGGGAGAATGTAATCATTCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGCCTGTCTTAGATGTCAAGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        754 BP; 206 A; 153 C; 202 G; 193 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAACAAACAAGAGGACTGTGTTGTTGTTGGGGGAGAATGTAATCATTCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                          LAMBERT CO
                                                                                                                                                                                                            98US-0099840
97US-0068179
                                                                                                                                                                                                                                             98WO-US26705
                                                                                                                                                                                                                                                                                                                               replace (157, T)
                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA; 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.3%;
                                                                                                                                                                                                                                                                                                           b
"C53S mutation"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 112; DB 20;
Pred. No. 2.2e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₿₽.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SAG)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene mutant
                                                                                                     related proteins, cells against apo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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                                                                                                     apoptosis
                                                                                                                 useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112
                                                                                                                 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             252
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This is the nucleotide sequence of human sensitive to apoptosis (SAG) mutant gene MM2, which codes for a SAG protein (see AAY06496) in which the Cys residue at position 53 of the native protein (see AAY06492) is replaced by a Ser residue owing to a mutation of codon 50 from TGC to AGC obtained by site-directed mutagenesis of SAG cDNA. This residue is at a haem binding site of SAG. Single and double SAG mutants (see AAX87317-31) were made in order to determine

determine

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RESULT 17
AAX87319
     PRINCE PR
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Best Local Simi
Matches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oligomerization. These properties were unaffected by the NM2 mutation. SAG is a novel zinc finger protein that promotes cell growth, protects cells from apoptosis, scavenges oxygen radicals and can be used for the reversion of a tumour phenotype. SAG genes, and mutant SAG genes, can be used to protect cells from apoptosis induced by redox reagents. They can also be used for the recombinant production of SAG proteins, which are molecular targets in the development of drugs against neurodegenerative disorders, cancers and muscle dystrophy, and promoting wound healing.
Claim 15; Page 62-63; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAG gene; sensitive to apoptosis; human; cancer; tumour; neurodegenerative disease; muscular dystrophy; wound healing;
                                                      promoting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human sensitive to apoptosis (SAG) gene mutant MM3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 754 BP; 206 A; 155 C; 201 G; 192 T; 0 other;
                                                                                                                                                                                                                                                                                                                                 11-SEP-1998;
19-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9932514-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX87319 standard; cDNA; 754 BP.
                                                                                                                                        P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vulnerary; therapy; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the role of each cysteine residue of SAG in haem binding and SAG
                                                                                                                                                                                                                                                                           (WARN ) WARNER
                                                Sensitive to Apoptosis Gene and oting cell growth and protecting
                                                                                                                                     1999-430152/36.
DB; AAY06497.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGTTGTGGTCTGGGGAGAATGTAATCATTCCTTCCACAACTGCTGC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGTTGTGGTCTGGGGAGAATGTAATCATTCCTTCCACAACTGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                           LAMBERT CO.
                                                                                                                                                                                                                                                                                                                              98US-0099840.
97US-0068179.
                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US26705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      replace(148,T)
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "C53S mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.3%;
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Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                related proteins, useful cells against apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .9e-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264
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RESULT 18
AAX87322
ID AAX87
XX AAX87
AC AAX87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is the nucleotide sequence of human sensitive to apoptosis (SAG) mutant gene MM3, which codes for a SAG protein (see AAY06497) in which the Cys residues at positions 50 and 53 of the native protein (see AAY06492) are replaced by Ser residues owing to mutations of codons 50 and 53 form TGC to AGC obtained by site-directed mutagenesis of SAG cDNA. These residues are at a haem binding site of SAG. Single and double SAG mutants (see AAX87317-31) were made in order to determine the role of each cysteine residue of SAG in haem binding and SAG oligomerization. MM3 showed greatly reduced haem binding and SAG oligomerization. MM3 showed greatly reduced haem binding and SAG oligomerization. MM3 showed greatly reduced haem binding and sAG oligomerization was unaffected. SAG is a novel zinc finger protein that promotes cell growth, protects cells from apoptosis, scavenges oxygen radicals and can be used for the reversion of a tumour phenotype. SAG genes, and mutant SAG genes, can be used to protect cells from apoptosis induced by redox reagents. They can also be used for the recombinant production of SAG proteins, which are molecular targets in the development of dyntrophy. and promoting wanted healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAG gene; sensitive to apoptosis; human; cancer; tumour; neurodegenerative disease; muscular dystrophy; wound healing; vulnerary; therapy; mutant; ds.
   WPI; 1999-430152/36.
                                                                                                                                                                                         11-SEP-1998;
19-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human sensitive to apoptosis (SAG) gene mutant MM6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX87322 standard; cDNA; 754 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 754 BP; 207 A; 155 C; 201 G; 191 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                            WO9932514-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-SEP-1999 (first entry)
                                                                                                                        (WARN )
                                                                                                                                                                                                                                                                                 15-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218
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                                                                                                                           WARNER LAMBERT CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGTTGTGGTCTGGGGAGAATGTAATCATTCCTTCCACAACTGCTGC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGAAAACAACAAGAGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                         98US-0099840
97US-0068179
                                                                                                                                                                                                                                                                                 98WO-US26705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 replace(244..246,CAT)
/*tag= b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1..342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "H82K mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
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Pred. No. 9.9e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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P-PSDB; AAY06500

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                            SAG gene; sensitive to apoptosis; human; cancer; tumour; neurodegenerative disease; muscular dystrophy; wound healing; vulnerary; therapy; mutant; ds.
15-DEC-1998;
                                        01-JUL-1999.
                                                                            WO9932514-A2
                                                                                                                                                               mutation
                                                                                                                                                                                                                           mutation
                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human sensitive to apoptosis (SAG) gene mutant MM10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oligomerization. These properties were unaffected by the MM6 mutation. SAG is a novel zinc finger protein that promotes cell growth, protects cells from apoptosis, scavenges oxygen radicals and can be used for the reversion of a tumour phenotype. SAG genes, and mutant SAG genes, can be used to protect cells from apoptosis induced by redox reagents. They can also be used for the recombinant production of SAG proteins, which are molecular targets in the development of drugs against neurodegenerative disorders, cancers and muscle dystrophy, and promoting wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is the nucleotide sequence of human sensitive to apoptosis (SAG) mutant gene MM6, which codes for a SAG protein (see AAY06500) in which the His residue at position 82 of the native protein (see AAY06492) is replaced by a Lys residue owing to a mutation of codon 82 from CAT to AAA obtained by site-directed mutagenesis of SAG CDNA. This residue is in zinc ring finger 1 of SAG. Single and double SAG mutants (see AAX87317-31) were made in order to determine the role of each cysteine residue of SAG in haem binding and SAG mutants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX87326 standard; cDNA; 754 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 15; Page 67-68; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201
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03; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                              /*tag= b
/note= "H85K mutation"
replace(253..255,CAC)
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/*tag= c
98WO-US26705
                                                                                                                                                                                                                     replace (244 . . 246, CAT)
                                                                                                                                                                                                                                                                                Location/Qualifiers
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100.0%; Pred. No. 1.3e-44;
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WO9932514-A2

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                                                                                                                                                                                             SAG gene; sensitive to apoptosis; human; cancer; tumour; neurodegenerative disease; muscular dystrophy; wound hea
                                                           mutation
                                                                                          CDS
                                                                                                                                                                                                                                         Human sensitive to apoptosis (SAG) gene mutant MM5
                                                                                                                                     Synthetic
                                                                                                                                                   Homo sapiens
                                                                                                                                                                                  vulnerary; therapy; mutant; ds.
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P-PSDB; AAY06504.
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19-DEC-1997;
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                                   /*tag= a
replace(238,T)
/*tag= b
/*tag= b
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97US-0068179.
                                                                                                   Location/Qualifiers
                           /note= "C80S mutation"
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100.0%;
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Pred. No. 1.3e-44;
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                                                                                                                                                                                             dystrophy; wound healing;
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RESULT 21
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Best Local S
Matches 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This is the nucleotide sequence of human sensitive to apoptosis (SAG) mutant gene MM5, which codes for a SAG protein (see AAY06499) in which the Cys residue at position 80 of the native protein (see AAY06492) is replaced by a Ser residue owing to a mutation of codon 80 from TGC to AGC obtained by site-directed mutagenesis of SAG CDNA. This residue is in zinc-ring finger 1 of SAG. Single and double SAG mutants (see AAX87317-31) were made in order to determine the role of each cysteine residue of SAG in haem binding and SAG colors and sag and SAG colors are the role of each cysteine residue of SAG in haem binding and SAG colors are the role of each cysteine residue of SAG in haem binding and SAG colors are the role of each cysteine residue of SAG in haem binding and SAG colors are the role of each cysteine residue of SAG in haem binding and SAG colors are the role of each cysteine residue of SAG in haem binding and SAG colors are the role of each cysteine residue of SAG in haem binding and SAG colors are the role of each cysteine residue of SAG in haem binding and SAG colors are the role of each cysteine residue of SAG in haem binding and SAG colors are the role of each cysteine residue of SAG in haem binding and SAG colors are the role of each cysteine residue of SAG in haem binding and SAG colors are the role of each cysteine residue of SAG in haem binding and SAG colors are the role of each cysteine residue of SAG in haem binding and SAG colors are the role of each cysteine residue of SAG in ham benefit and the role of each cysteine residue of sAG colors are the role of each cysteine residue of sAG colors are the role of each cysteine residue of sAG colors are the role of each cysteine residue of sAG colors are the role of each cysteine residue of sAG colors are the role of each cysteine residue of sAG colors are the role of each cysteine residue of sAG colors are the role of each cysteine residue of sAG colors are the role of each cysteine residue of sAG colors are the role of each cysteine residue of sAG col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oligomerization. These properties were unaffected by the MMS mutation. SAG is a novel zinc finger protein that promotes cell growth, protects cells from apoptosis, scavenges oxygen radicals and can be used for the reversion of a tumour phenotype. SAG genes, and mutant SAG genes, can be used to protect cells from apoptosis induced by redox reagents. They can also be used for the recombinant production of SAG proteins, which are molecular targets
                                                                                                                                                                                     SAG gene; sensitive to apoptosis; human; cancer; tumour; neurodegenerative disease; muscular dystrophy; wound hea volnerary: therapy; mutant; colon carcinoma; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                 Human sensitive to apoptosis (SAG)
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19-DEC-1997;
                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX87315 standard; cDNA; 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 15; Page 66; 84pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 78.2%;
Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   754 BP; 206 A; 155 C; 201 G; 192 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAACAAACAAGAGGACTGTGTTGTGGTCTGGGGAGAA 237
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97US-0068179.
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                                                Location/Qualifiers
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Pred. No.
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                                                                                                                                                                                                               wound healing;
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RESULT 22
AAH25847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in SAG RNA, but not in genomic DNA. It suggests a possible role for SAG in human carcinogenesis. SAG genes, and mutant SAG genes, can be used to protect cells from apportosis induced by redox reagents. Antisense SAG genes can be used to inhibit the growth of tumour cells. The SAG genes can also be used for the recombinant production of the SAG proteins. The SAG proteins can be used to scavenge oxygen radicals in organisms and to promote wound healing. Additionally, the SAG genes or their complements can be used to promote or inhibit the growth of plant cells (all claimed). The SAG protein is also an ideal molecular target in the development of the SAG genes or their complements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human sensitive to apoptosis gene SAG (see also AAX87314). The cDN was obtained by PCR amplification of RNA isolated from DLD-1 colon carcinoma cells (ATCC CCL 221). It contains a 7 bp deletion compared with native SAG, starting at nucleotide 170 of the coding region that codes for a potential haem binding site. The frame shift deletion abolishes the downstream zinc finger in the resulting protein (see AAY66493). The mutation was detected by PCR resulting protein (see AAY66493).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAG: Sensitive to Apoptosis Gene and related proteins, useful for promoting cell growth and protecting cells against apoptosis
                                                              Human; apoptosis associated protein 12; SAG protein 12; haemopathy; HIV infection; immunological disease; inflam
                                                                                                                 Human apoptosis associated protein 12 coding sequence.
                                                                                                                                                                                                                 AAH25847 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           drugs against neurodegenerative disorders, dystrophy.
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P-PSDB; AAY06493.
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19-DEC-1997;
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                                                                                                                                                                                    AAH25847;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (WARN ) WARNER LAMBERT CO
                                                                                                                                                                                                                                                                                                                                                                      168
                                                                                                                                                                                                                                                                                                       228
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                                                                                                                                                                                                                                                                                                                              95 GAATGTAATCATTCCTTCCACAACTGCTGC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                     90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                      GATGCCTGTCTTAGATGTCAAGCTGAAAACAAACAAGAGGACTGTGTTGTTGGTCTGGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP; 204 A; 155 C; 197 G; 191 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54-55; 84pp; English.
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97US-0068179
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                                                                                                                                                                                                                   DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.6%; Score 90; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 20; 1
9.7e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancers and muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                       ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 747;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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WO200132863-A1

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ARESULT 23
AAX87320
ID AAX87
XX AAX87
AC AAX87
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Best Local S
Matches 89
11-SEP-1998;
19-DEC-1997;
                                                                                                                                 01-JUL-1999.
                                                                                                                                                                                         WO9932514-A2
                                                                                                                                                                                                                                                                                                 mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAG gene; sensitive to apoptosis; human; cancer; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human sensitive to apoptosis (SAG) gene mutant MM4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides the protein and coding sequences of human apoptosis associated (SAG) protein 12. These sequences can be used in the diagnosis and treatment of malignant tumours, haemopathy, HIV infection, immunological diseases and various types of inflammation. The present sequence is the SAG protein 12 coding sequence.
                                                                              15-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vulnerary; therapy; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neurodegenerative disease; muscular dystrophy; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAX87320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX87320 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human apoptosis associated protein 12 and encoded polynucleotide, applicable in diagnosis and treatment of malignant tumour, hemopathy, HIV infection, immunological diseases and various inflammation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 22-23; 27pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-335831/35.
)B; AAB98975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            564 ATGCCTGTCTTAGATGTCAAGCTGAAAAACAAACAAGAGGACTGTGTTGTGGTCTGGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 AATGTAATCATTCCTTCCACAACTGCTGC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 ATGCCTGTCTTAGATGTCAAGCTGAAAAAAAAAAAAGAGGACTGTGTTGTGGTCTGGGGAG 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATGTAATCATTCCTTCCACAACTGCTGC 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1152 BP; 292 A; 265 C; 309 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.8%; Score 89; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
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98US-0099840
97US-0068179
                                                                              98WO-US26705
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                                                                                                                                                                                                                                                                  replace(181,T)
/*tag= b
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1..342
                                                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                      note= "C61S mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22; I
3.2e-37;
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RESULT 24
AAX87328
PD XXX
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Best Local S
Matches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oligomerization. These properties were unaffected by the MM4 mutation. SAG is a novel zinc finger protein that promotes cell growth, protects cells from apoptosis, scavenges oxygen radicals and can be used for the reversion of a tumour phenotype. SAG genes, and mutant SAG genes, can be used to protect cells from apoptosis induced by redox reagents. They can also be used for the recombinant production of SAG proteins, which are molecular targets in the development of drugs against neurodegenerative disorders, cancers and muscle dystrophy, and promoting wound healing.
                                                                                                                                                      Key
                                                                                                                                                                                                                                                                                                                                                                                                               AAX87328 standard; cDNA; 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This is the nucleotide sequence of human sensitive to apoptosis (SAG) mutant gene MM4, which codes for a SAG protein (see AAY06498) in which the Cys residue at position 61 of the native protein (see AAY06492) is replaced by a Ser residue owing to a mutation of codon 50 from TGC to AGC obtained by site-directed mutagenesis of SAG CDNA. This residue is at zinc-ring finger 1 of SAG. Single and double SAG mutants (see AAX87317-31) were made in order to determine the role of each cysteeine residue of SAG in them banding and SAG colors.
                                WO9932514-A2
                                                                                                  mutation
                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                        SAG gene; sensitive to apoptosis; human; neurodegenerative disease; muscular dystr
                                                                                                                                                                                                                                                                                                           Human sensitive to apoptosis
                                                                                                                                                                                                                                                                                                                                               27-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                  AAX87328;
                                                                                                                                                                                                                                      vulnerary; therapy; mutant; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAG: Sensitive to Apoptosis Gene and related proteins, useful promoting cell growth and protecting cells against apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-430152/36.
P-PSDB; AAY06498.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 GTCTTAGATGTCAAGCTGAAAACAAACAAGAGGACTGTGTTGTGGTCTGGGGAGAATGTA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCATTCCTTCCACAACTGCTGC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCTTAGATGTCAAGCTGAAAACAAACAAGAGGACTGTGTTGTGGTCTGGGGAGAATGTA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  754 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCATTCCTTCCACAACTGCTGC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.9%; Score 83; llarity 100.0%; Pred. No. Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                /*tag= a
replace(217,T)
                                                                                                                                    Location/Qualifiers
1..342
                                                               /note= "C73S mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206 A; 155 C; 201 G; 192 T; 0 other;
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                                                                                                                                                                                                                                                      muscular dystrophy; wound healing
                                                                                                                                                                                                                                                                                                       (SAG) gene mutant MM12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.9e-34;
                                                                                                                                                                                                                                                                         cancer; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 754;
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01-JUL-1999

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RESULT 25
AAX87327
ID AAX87
    FT FT FT XXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SAG) mutant gene MM12, which codes for a SAG protein (see AAV06506)

Cin which the Cys residue at position 73 of the native protein (see AAV06492) is replaced by a Ser residue owing to a mutation of codon 73 from TGT to AGC obtained by site-directed mutagenesis of SAG CDNA. This residue is in a protease inhibitor movif of SAG. Single and double SAG mutants (see AAX87317-31) were made to determine the role of each cysteine residue of SAG in haem binding and SAG oligomerization. These properties were unaffected by the MM12 mutation. SAG is a novel zinc finger protein that promotes cell growth, protects cells from apoptosis, scavenges oxygen radicals and can be used for the reversion of a tumour phenotype. SAG genes, and mutant SAG genes, can be used to protect cells from apoptosis induced by redox reagents. They can also be used for the recombinant production of SAG proteins, which are molecular targets in the development of drugs against neurodegenerative disorders,
                 mutation
                                                                                        Homo sapiens.
Synthetic.
                                                                                                                                                  SAG gene; sensitive to apoptosis; human; cancer; tumour; neurodegenerative disease; muscular dystrophy; wound hea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 754 BP; 206 A; 155 C; 201 G; 192 T; 0 other;
                                                                                                                                                                                          Human sensitive to apoptosis (SAG) gene mutant MM11.
                                                                                                                                                                                                                             27-SEP-1999
                                                                                                                                                                                                                                                          AAX87327;
                                                                                                                                                                                                                                                                                     AAX87327 standard; cDNA; 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is the nucleotide sequence of human sensitive to apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAG: Sensitive to Apoptosis Gene and related proteins, useful promoting cell growth and protecting cells against apoptosis
                                                                                                                                  vulnerary; therapy; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancers and muscle dystrophy, and promoting wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 15; Page 77-78; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-430152/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-SEP-1998;
19-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                         141
                                                                                                                                                                                                                                                                                                                                                                201
                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76;
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY06506.
                                                                                                                                                                                                                                                                                                                                                                                            AAACAAACAAGAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                        CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
                                                                                                                                                                                                                                                                                                                                                              AAACAAACAAGAGGAC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                           (first entry)
/*tag= a
replace(190,T)
/*tag= b
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97US-0068179
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                                             1..342
                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.3%;
                                                                                                                                                                                                                                                                                                                                                                                        76
                                                                                                                                                muscular dystrophy; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ٥,
                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 76;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 20; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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AAX87329
ID AAX87329
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AC AAX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SAG) mutant gene MM11, which codes for a SAG protein (see AAY06505)

(in which the Cys residue at position 64 of the native protein (see AAY06492) is replaced by a Ser residue owing to a mutation of codon 64 from TGT to AGC obtained by site-directed mutagenesis of SAG cDNA. This residue is in zinc-ring finger 1 of SAG. Single and double SAG mutants (see AAX87317-31) were made in order to determine the role of each cysteine residue of SAG in haem binding and SAG mutantion. These properties were unaffected by the MM11 mutation. SAG is a novel zinc finger protein that promotes cell growth, protects cells from apoptosis, scavenges oxygen radicals and can be used for the reversion of a tumour phenotype. SAG genes, and mutant SAG genes, can be used to protect cells from apoptosis induced by redox reagents. They can also be used for the recombinant production of SAG proteins, which are molecular targets in the development of drugs against neurodegenerative disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local (
                               Synthetic
                                                                                                                                           SAG gene; sensitive to apoptosis; human; cancer; tumour; neurodegenerative disease; muscular dystrophy; wound healing;
                                                                                                                                                                                                                                                                                                         27-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 754 BP; 206 A; 155 C; 201 G; 192 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAG: Sensitive to Apoptosis Gene and related proteins, useful promoting cell growth and protecting cells against apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-430152/36.
P-PSDB; AAY06505.
                                                            Homo sapiens.
                                                                                                                 vulnerary; therapy; mutant; ds.
                                                                                                                                                                                                                                       Human sensitive to apoptosis (SAG) gene mutant MM13
                                                                                                                                                                                                                                                                                                                                                                                                                              AAX87329 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is the nucleotide sequence of human sensitive to apoptosis (SAG) mutant gene MM11, which codes for a SAG protein (see AAY06505)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 15; Page 76; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sun Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-SEP-1998;
19-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9932514-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and muscle dystrophy, and promoting wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCACAACTGCTGC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCAAGCTGAAAACAAACAAGAGGACTGTGTTGTTGTTGGGGGGAGAATGTAATCATTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCAAGCTGAAAACAAACAAGAGGACTGTGTTGTGGTCTGGGGGAGAATGTAATCATTCCT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCACAACTGCTGC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0099840.
97US-0068179.
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                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA; 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 74;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                 ₽P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.8e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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CDS

Location/Qualifiers

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SAXAXI
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                                                                                                                                                                                                                                                                                                           AAX41085
                                                                                             RESULT 27
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                                                                                                                                                                                                                                                                                                                                          This is the nucleotide sequence of human sensitive to apoptosis (SAG) mutant gene MM13, which codes for a SAG protein (see AAY06507) in which the Cys residues at positions 61 and 64 of the native protein (see AAY06422) are replaced by Ser residues owing to mutations of codons 61 and 64 through site-directed mutagenesis of SAG cDNA. These residues are in zinc ring finger 1 of SAG. Single Couble SAG mutants (see AAX87317-31) were made in order to determine the role of each cysteine residue of SAG in haem binding and SAG oligomerization. MM13 showed greatly reduced haem binding (and a cereased brown colour) but oligomerization was unaffected. SAG is a novel zinc finger protein that promotes cell growth, protects cells from apoptosis, scavenges oxygen radicals and can be used for the reversion of a tumour phenotype. SAG genes, and mutant SAG genes, can be used to protect cells from apoptosis induced by redox reagents. They can also be used for the recombinant production of SAG proteins, which are molecular targets in the development of drugs against neurodegenerative disorders, cancers and muscle
                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
             18-JUN-1999
                                       AAX41085;
                                                                AAX41085
                                                                                                                                                                                                                                                                                                         Sequence 754 BP;
                                                                                                                                                                                                                                                                                                                                    dystrophy, and promoting wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   promoting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-430152/36
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19-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mutation
                                                                                                                                                                  111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sensitive to Apoptosis Gene and related proteins, useful oting cell growth and protecting cells against apoptosis
                                                                                                                                        251
                                                                                                                                                                                              191
                                                                                                                                                                                                                         51
                                                                                                                                                                                                                                                  74;
                                                                                                                                                                  TCCACAACTGCTGC
                                                                  standard;
                                                                                                                                       TCCACAACTGCTGC 264
                                                                                                                                                                                             GTCAAGCTGAAAACAAACAAGAGGACTGTGTTGTGGTCTGGGGAGAATGTAATCATTCCT
                                                                                                                                                                                                                 GTCAAGCTGAAAACAAGCAAGAGGACTGTGTGTGTGGGGGAGGAATGTAATCATTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 79-80; 84pp; English.
                                                                                                                                                                                                                                                   Conservative
           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAMBERT CO
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97US-0068179.
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                                                                                                                                                                                                                                                                                                        207 A; 155 C; 201 G; 191 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               replace (190, T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "C64S mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "C61S mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag=
                                                                cDNA; 224
                                                                                                                                                                                                                                            59.7%; 5
100.0%; Pr
                                                                                                                                                                  124
                                                                                                                                                                                                                                                Score 74; DB; Pred. No. 2.8
                                                                  ВP
                                                                                                                                                                                                                                                             DB 20; I
2.8e-29;
                                                                                                                                                                                                                                                                           Length 754;
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                Gaps
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RESULT 28
AAX87316
                                                                                                                                                                                                                                                                                                                                                                             cc human secreted proteins, and encode the proteins given in AAV01602 and candidate to AAV11994 to AAV12260, respectively. The proteins given represent the cc signal peptide and an N-terminal fragment of a secreted protein. The cc nucleic acid sequences can be used for producing secreted human gene cc products. They can also be used to develop products for diagnosis and cc therapy. The proteins obtained may have cytokine activity, cell cc proliferation/differentiation activity, haematopoiesis regulating cc activity, tissue growth regulating activity, reproductive hormone cr regulating activity, chemotactic/chemokinetic activity, haematory cativity, the products can decrease the used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into
                                                                                                                                                                                                            밁
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                                                                                                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                                                                                                                                         Query Match
                            Human sensitive to
                                                                                             AAX87316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acids encoding human secreted proteins - obtained cDNA libraries prepared from kidney, fetal kidney, dystrophic muscle, muscle and heart tissue
                                                            27-SEP-1999
                                                                                                                           AAX87316 standard; cDNA; 706
                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                         a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAY12252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9906554-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haemacopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-153784/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thrombolytic; anti-inflammatory; tumour inhibition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human;
                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                            164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      secreted protein 5'
                                                                                                                                                                                                                                                                         43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         secreted
                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                         CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGT 206
                                                                                                                                                                                                                                       CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGT 43
                                                                                                                                                                                                                                                                                                                                         224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 441; 622pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dumas
                                                                                                                                                                                                                                                                                                                                        B₽;
                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0905134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; EST; expressed sequence tag; diagnosis;
                                                                                                                                                                                                                                                                                                                                      41 A; 60 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Milne Edwards
                           apoptosis
                                                                                                                                                                                                                                                                                       34.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST SEQ ID NO:
                                                                                                                                                                                                                                                                       0,
                                                                                                                           ВP
                                                                                                                                                                                                                                                                                       Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                      83 G; 38 T; 2 other;
                            (SAG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>,</u>
                                                                                                                                                                                                                                                                         Mismatches
                           gene mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lacroix B;
                                                                                                                                                                                                                                                                                       DB 20; Length 224; 7e-13;
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                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                      0,
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                                                                                                                                                                                                                                                                      Gaps
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SAG gene; sensitive to apoptosis; human; cancer; tumour;

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      XXXXXXXX
                                                                                                                                                        AAC7
                                                                                                                                                                      RESULT 29
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                                                                                                                                                                                                                                                                                                                                                                                                  human sensitive to apoptosis gene SAG (see also AAX87314). The CDNA was obtained by PCR amplification of RNA isolated from DLD-1 colon carcinoma cells (ATCC CCL 221). It contains a 48 bp deletion compared with native SAG, starting at nucleotide 177 of the coding region that codes for a potential haem binding site. The in-frame deletion eliminates 16 amino acids in the encoded protein (see AAY06494) but retains the zinc finger motif. The mutation was detected by PCR in SAG RNA, but not in genomic DNA. It suggests a possible role for SAG in human carcinogenesis. SAG genes, and mutant SAG genes, can be used to protect cells from apoptosis induced by redox reagents. Antisense SAG genes can also be used for the recombinant production of the SAG genes can also be used for the recombinant production of the SAG genes or their complements can be used to scavenge oxygen radicals in organisms and to proteins can be used to proteins or the SAG genes or their complements can be used to promote or inhibit the growth of plant cells (all claimed). The SAG protein is also an ideal molecular carget in the development of drugs against neurodegenerative
                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                               Human ORFX ORF3048 polynucleotide sequence SEQ ID NO:6095
Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                          Sequence 706 BP; 189 A; 147 C; 189
                                                                     08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAG: Sensitive to Apoptosis Gene and related proteins, useful promoting cell growth and protecting cells against apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-430152/36.
P-PSDB; AAY06494.
                                                                                                                                    AAC77493 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                         disorders, cancers and muscle dystrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is the nucleotide sequence of deletion mutant 2 of the novel human sensitive to apoptosis gene SAG (see also AAX87314). The c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 15; Page 55-56; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-SEP-1998;
19-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurodegenerative disease; muscular dystrophy; wound healing; vulnerary; therapy; mutant; colon carcinoma; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (WARN ) WARNER LAMBERT CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                          83 GTGGTCTGGGGAGAATGTAATCATTCCTTCCACAACTGCTGC 124
                                                                                                                                                                                                                                                                                         42;
                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                      GTGGTCTGGGGAGAATGTAATCATTCCTTCCACAACTGCTGC 216
                                                                                                                                                                                                                                                                                           Conservative
                                                                     (first entry)
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97US-0068179
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1..294
/*tag= a
                                                                                                                                                                                                                                                                                                     33.9%;
                                                                                                                                      441
                                                                                                                                                                                                                                                                                     Score 42; DB; Pred. No. 2.3
                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                        G; 181 T; 0 other;
                                                                                                                                                                                                                                                                                                       .3e-12;
                                                                                                                                                                                                                                                                                                                          20;
                                                                                                                                                                                                                                                                                                                     Length 706;
                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                       0
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208 GTGGTCTGGGGAGAATGTAATCATTCCTTCCACAACTGCTG 248 GTGGTCTGGGGAGAATGTAATCATTCCTTCCACAACTGCTG Matches

Conservative

0;

Query Match Best Local Similarity

33.1%;

Score 41; Pred. No. Mismatches

DB 21; 1 . 7.9e-12;

Length 441; Indels

0,

Gaps

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antipsoriatic; antiparkinsonian; nootropic; neuroprotective; costeopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; cosqulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The mucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, thypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, allowed the combined immunodeficiency (SCID) as thems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; altergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
Sequence
                                                                                                                                            bacterial or fungal infection, malaria, autoimmune disorders, a allergies, aplastic anaemia, burns, wounds, bone and cartilage on nocturnal haemoglobinuria, antiinflammatory disease; to enhance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Page 5279; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anticonvulsant; osteopathic; antiarthritic; immunosuppressant; card: immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antiviral; antibacterial; antique antippressive; antithyroid;
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05-APR-1999;
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                                                                                                  coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAB43284.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vulnerary; antipsoriatic; antiparkinsonian;
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441 BP;
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99US-0127728
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                                                                                             inhibit thrombosis; and as a contraceptive
98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  z
A; 113 C; 139 G; 90 T; 1 other;
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RESULT 30
ABN40537
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                                                                                                                                                                        set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised minicular biological or pathological state, and so allowing the condition of tissue- and pathological state, and so allowing the condition; to detect developmental specific genes such as those genes condition; to detect developmental specific genes and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent othe exemplification of the present invention.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                               Query Match
Best Local S
Matches 35
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splice
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human spliced transcript detection oligonucleotide SEQ ID NO:13285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABN40537 standard; DNA; 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription a genome, useful for detecting tissue-, pathology-, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABN40537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUL-2000; 2000US-221607P.
02-MAY-2001; 2001US-287724P.
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                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; SEQ ID 13285; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        developmental-specific genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (COMP-) COMPUGEN INC
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variant;
26
                                                                35;
                                                                                Similarity
                                                                                                                               60
                    CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGG 35
 CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wasserman
                                                                                                                              B₽;
                                                                Conservative
                                                                                                                                                           .int/pub/published_pct_sequences
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t; transcriptome; oligonucleotide library; ss.
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                                                                                                                              A; 13 C;
                                                                              28.2%;
100.0%;
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                                                                0;
                                                                                Score 35;
Pred. No.
                                                                                                                              G; 12 T; 0 other;
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                                                                Mismatches
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                                                                                                 DB 24;
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 60
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                                                                                             Length
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CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGG

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Query Match
Best Local S
Matches 35
                                                                                                                                                                                                                                             nucleotide sequence selected from any of 948 sequences.

(ABZ11119-ABZ12066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful for identifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight markers, as a food supplement, for generating antibodies, in medical imaging, screening and diagnostic assays and for treating cell-proliferative disorders (cancer), neurodegenerative diseases (multiple sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid disorders, platelet or coagulation disorders, wound, burns, incision, ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal, parasitic), arthitits, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet or coagulation disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; genome mapping; gene therapy; food supplement; virus; cell-proliferative disease; bacte: cell-proliferative disease; bacte: Parkinson's disease; Albeimer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABZ11414;
                                                                                                               Sequence
                                                                                                                                                                     Note: The sequence data for this patent did not specification, but was obtained in electronic fo at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-MAR-2001; 2001US-0799451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-MAR-2002; 2002WO-US05095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiarthritic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human polynucleotide SEQ ID NO 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated polynucleotide (I) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-759812/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         haemostatic; vulnerary; fungicide; antibacterial; virucide;
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T, Wang J,
                              Similarity
                                                                                                                     439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 296; 1012pp + Sequence Listing;
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Yang Y,
   28.2%;
ilarity 100.0%;
Conservative (
                                                                                                                  B₽;
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                                                                                                                     69
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Ma Y, Yamazaki V, Chen R,
J, Wang D, Drmanac RT;
                                                                                                                  A; 142 C; 162 G;
   Score 35; DB; Pred. No. 1.2
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                                                                                                                     66 T; 0 other;
                                                            DB 24;
                                    1.2e-08;
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format
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Wang
                                                            Length 439;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77
                                                                                                                                                                                                         part of the printed directly from WIPO
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Ghosh
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RESULT 32
AAX87313
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                                                                                              This is the nucleotide sequence of mouse sensitive to apoptosis (SAG) cDNA, which codes for a novel redox sensitive, haem-binding protein (see AAY06491) with a zinc RING finger domain that promotes cell growth, protects cells from apoptosis, scavenges oxygen radicals and can be used for the reversion of a tumour phenotype. The cDNA was isolated using differential display to identify genes associated with 1,10-phenanthroline (OP)-induced apoptosis in murine tumour lines, and use of an isolated OP-inducible clone to screen a mouse lung cDNA library. The mouse SAG cDNA was used to identify human SAG (see AAX87314). SAG is highly conserved among species. Disruption in yeast was shown to be lethal. SAG deletion mutants (see AAX87315-16) have been identified in human cancer lines, suggesting a role in carcinogenesis. SAG genes, and mutant SAG genes, can be used to protect cells. The SAG genes can be used to inhibit the growth of the SAG genes san also be used for the recombinant production of the SAG genes can also be used for the recombinant of the SAG genes can also be used for the recombinant of the SAG genes can also be used for the recombinant the sadditionally, the SAG genes or their complements can be used to protein is also an ideal molecular target in the development of drugs against neurodegenerative disorders, cancers and muscle
                               Matches
                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAG: Sensitive to Apoptosis Gene and related proteins, useful promoting cell growth and protecting cells against apoptosis
                                                                                              Sequence 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 48-49; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-SEP-1998;
19-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-430152/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (WARN ) WARNER LAMBERT CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vulnerary; therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neurodegenerative disease; muscular dystrophy; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAG gene; sensitive to apoptosis; mouse; cancer; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse sensitive to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX87313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX87313 standard; cDNA; 1140 BP
                             Local Similarity nes 32; Conserv
11 GCCATCTGCAGGGTCCAGGTGATGGATGCCTG 42
                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                           BP; 302 A; 224 C; 287 G; 327 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0099840
97US-0068179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-US26705
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                        25.
100.0%; F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        b
                                              Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SAG)
                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene.
                                            4.5e-07;
                                                             DB 20;
                                                           Length 1140;
                               Indels
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                             Gaps
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RESULT 34
AAL25052
ID AAL25
XX
AC AAL25
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AC O7-DE
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DT 07-DE
XX
DE Humar
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                                                                                                                                                                                                    Matches
                                                                                                                                                                                                             Query Match
Best Local Similarity
                                    07-DEC-2001
                                                                                                                                                                                                                                                 Sequence 264
                                                                                                                                                                                                                                                                                     The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
                                                                                                                                                                                                                                                                                                                                        The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells.
           Human breast cancer expressed polynucleotide 17509
                                                             AAL25052;
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 1568; 3695pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                              New peptide useful as a marker for the diagnosis of breast cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAR-2000; 2000US-0189167.
24-MAR-2000; 2000US-0192099.
29-MAR-2000; 2000US-0193480.
15-MAY-2000; 2000US-0205230.
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                                                                                      AAL25052 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-451856/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lillie J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JAN-2000; 2000US-0176077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; breast cancer; cell marker; cytostatic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAL16209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAL16209 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-JAN-2001; 2001WO-US00798
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                                                                                                                                                                           101
                                                                                                                                                                                                 24;
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                                                                                                                                                   54
                                                                                                                                                                  AATCATTCCTTCCACAACTGCTGC 124
                                                                                                                                                   AATCATTCCTTCCACAACTGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xu Y,
                                                                                                                                                                                                  Conservative
                                   (first entry)
                                                                                                                                                                                                                                                 BP; 64 A; 59 C;
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2000US-0220534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA;
                                                                                     CDNA; 596
                                                                                                                                                                                                             19.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expressed polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Steinmann
                                                                                                                                                                                                  0
                                                                                                                                                                                                             Score 24;
Pred. No.
                                                                                                                                                                                                                                                 74 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₽P
                                                                                                                                                                                                  Mismatches
                                                                                                                                                   77
                                                                                                                                                                                                                                                 62 T; 5 other;
                                                                                                                                                                                                             DB 22;
0.0078;
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RESULT 35
AAL22239
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14-MAR-2000; 2000US-0189167.
24-MAR-2000; 2000US-01992099.
29-MAR-2000; 2000US-0199480.
15-MAY-2000; 2000US-0295330.
09-JUN-2000; 2000US-0213115.
25-JUL-2000; 2000US-0220534.
 14-JAN-2000;
14-MAR-2000;
24-MAR-2000;
29-MAR-2000;
                                                                                                WO200151628-A2
                                                                                                                                            Human; breast
                                                                                                                                                               Human breast cancer expressed polynucleotide 14696
                                                                                                                                                                                      07-DEC-2001
                                                                                                                                                                                                            AAL22239;
                                                                                                                                                                                                                                                                                                                                                                             Sequence 596 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; breast cancer; cell marker; cytostatic; ss.
                                                                          19-JUL-2001
                                                                                                                                                                                                                                  AAL22239
                                                                                                                                                                                                                                                                                                                                                                                                        detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encode polypeptides are also useful for isolating compounds with cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptide useful as a marker for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUL-2001
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                                                    10-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                          The polynucleotides and encoded polypeptides are potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-JAN-2001; 2001WO-US00798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                           101
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                                                                                                                                                                                                                                                                                                                                 24;
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                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                 AATCATTCCTTCCACAACTGCTGC 124
                                                                                                                                                                                                                                 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 3235;
                                                                                                                                                                                                                                                                                       AATCATTCCTTCCACAACTGCTGC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xu Y,
; 2000US-0176077.
; 2000US-0189167.
; 2000US-0192099.
; 2000US-0193480.
                                                                                                                                                                                                                                                                                                                                19.4%;
ilarity 100.0%;
Conservative (
                                                    2001WO-US00798
                                                                                                                                                                                     (first
                                                                                                                                            cancer;
                                                                                                                                                                                                                                                                                                                                                                          166 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang
                                                                                                                                                                                                                                 CDNA; 630
                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3695pp;
                                                                                                                                         cell marker; cytostatic; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ۲
                                                                                                                                                                                                                                                                                                                                                                          124 C; 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Steinmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                 ВP
                                                                                                                                                                                                                                                                                                                                             Score 24;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                          G; 162 T; 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis
                                                                                                                                                                                                                                                                                                                                           DB 22;
0.0077;
                                                                                                                                                                                                                                                                                                                                 0
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                                                                                                                                                                                                                                                                                                                                                                            other;
                                                                                                                                                                                                                                                                                                                                                      Length 596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of breast
                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     and encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                            markers for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer
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RESULT 36
AAA70390/c
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Best Local S
Matches 24
                                                                                                         Hall
                                                                                                                                                                                                                                                                                     Mucociliary dysfunction; mucus; sputum; human; chronic obstructive lung disease; chronic boronchitis; CB; Bronchiectasis; BE; asthma, cystic fibrosis; CF; bacterial infection; placental bikunin; Kunitz-type serine protease inhibitor; chronic sinusitis; glue ear; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human breast cancer expressed poly (AAL07544-AAL26789) and methods of assessing whether a pati affilicted with breast cancer by examining the correlation texpression of certain markers and the cancerous state of brine polynucleotides and encoded polypeptides are potential
                               Stimulating mucociliary clearance rate of mucus and sputum in lung airways for treating lung diseases such as cystic fibrosis and bronchitis involves administering a Kunitz-type serine protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encode polypeptides are also useful for isolating compounds with cytostatic
                                                                                                                                                       22-DEC-1998;
17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                   Site directed mutagenesis oligonucleotide # 1 for placental bikunin.
                                                                                                                                                                                                                                                                                                                                                                            02-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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09-JUN-2000;
                                                                                WPI; 2000-452127/39
                                                                                                                                                                                           22-DEC-1999;
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                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                         AAA70390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide useful as a marker
                                                                                                        ₽,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24;
                                                                                                         Pol1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATCATTCCTTCCACAACTGCTGC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   630
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                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATCATTCCTTCCACAACTGCTGC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     č
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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2000US-0211315.
2000US-0220534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP;
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                                                                                                        CI,
                                                                                                                                AG
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                                                                                                                                                       98US-0218913
99US-0441966
                                                                                                                                                                                          99WO-GB04381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213 A; 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang
                                                                                                         Newton
                                                                                                                                                                                                                                                                                                                                                                                                                         DNA; 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.4%;
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                                                                                                         ВВ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 24;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDICINE INC
                                                                                                        Taylor WJA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for the diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
0.0077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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patient is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and encoded
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         markers for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Example 9; Page 59; 173pp; English

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RESULT 37
AXX87337
ID AAXX87
XX AXX87
XX AXX87
XX AXX87
XX AXX87
XX AXX67
XX SAG 9
KW POULT
XX POWN
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 19
                     Primer hSAG.M1 corresponds to nucleotides 151-171 of the human sensitive to apoptosis gene (SAG) cDNA clone provided in AAX87314. It was used with primer SAGT.02-1 (see AAX87338) in the RT-PCR amplification of RNA isolated from 20 human tumour lines and transformed lines originating from lung, brain, kidney, prostate, testis, nasopharynx, bone, cervix and foreskin. 2 SAG deletion mutants (see AAX87315-16) were detected in cancer cell lines
                                                                                                                                                                                                                                                                                                                          SAG: Sensitive to Apoptosis Gene and related proteins, useful promoting cell growth and protecting cells against apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-SEP-1998;
19-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human sensitive to apoptosis gene (SAG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAX87337
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                                                                                                                                                                                                                                                                    Example 13; Page 26; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-430152/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (WARN ) WARNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vulnerary; therapy; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence of AAB14190.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38
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19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; DNA; 18 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACGTGCGCCATCTGCAGGG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACGIGCGCCATCIGCAGGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP; 4 A;
   from colon and testis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAMBERT CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0099840.
97US-0068179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98WO-US26705.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; 18 G; 8 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    muscular dystrophy; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 19;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primer hSAG.M1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 45;
possible role for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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GGGAGAATGTAATCATTC 108

Matches Query Match Best Local

Local Similarity 18;

> 100.0%; 14.5%;

> Score 18; Pred. No.

DB

21;

Length 349;

Conservative

0;

Mismatches

<u>.</u>

Indels

0;

Gaps

0

Sequence 349 BP; 101 A; 65 C; 67 G;

116 T; 0 other;

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RESULT 38
AAC29980/c
ID AAC299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                      sequences usually correspond mainly to the 3 untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                      New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 redox-sensitive, haem-binding protein that promotes cell growt
protects cells from apoptosis, and scavenges oxygen radicals.
                                                                                                                                                                               mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
                                                                                                                                                                                                                                                            Claim 1; SEQ ID 34055; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                     Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP1033401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted protein 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC29980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC29980 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 BP; 3 A; 6 C; 6 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAG in human carcinogenesis.
                             expression
                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-500381/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-FEB-2000; 2000EP-0200610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; 5' EST; expressed sequence tag;
                                                                                                                                                                                                                              The present sequence is one of a large number of 5' ESTs derived from
                                                                                                                                                                                                                                                                                                                                                                                                                      (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCATCTGCAGGGTCCAG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCATCTGCAGGGTCCAG 18
                             and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to reverse a tumour phenotype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA; 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.5%;
                                                                                                                                                                                                                                                                                                                                                                                     Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAG (see also AAY06492) is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO: 34055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       Giordano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              growth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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RESULT 39
ABV87139/c
ID ABV87139 standard;
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AAQ70827/c
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Best Local S
Matches 18
                                                                                                                                                                                                                                                                      The invention relates to a human colon tumour expressed polynucleotide (II, angel) encoding a polypeptide (II, ABB679991-ABB679996) comprising; (i) any of 2600 fully defined nucleotide sequences (ABV8669-ABV89289); (ii) complements of (i); (iii) at least 20 contiguous residues of (i); (iv) sequences that hybridize to (i); under moderately stringent conditions; (v) sequences having at least 75% or 90% identity to (i); or (vi) sequences having at least 75% or 90% identity to (i); or (vi) degenerate variants of (i). The compositions and methods of the present invention are useful for the diagnosis, prevention and/or treatment of cancer, particularly colon cancer. (I) can be used in gene therapy and (II) and (II) are useful in pharmaceutical compositions such as vaccines. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; colon; cancer; cytostatic; tumour; gene therapy; vaccine; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABV87139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-NOV-2000; 2000US-25222P.
66-FEB-2001; 2001US-257011P.
28-MAR-2001; 2001US-279670P.
10-JUL-2001; 2001US-304037P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated tumor colon polynucleotide and polypeptide, useful diagnosis, prevention and/or treatment of cancer, in particular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200258534-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human colon cancer related cDNA
                                                                                                                                                                                                                                Sequence 541 BP; 173 A; 99 C; 105 G; 164 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-608400/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-NOV-2001; 2001WO-US43704.
             AAQ70827;
                                          AAQ70827 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                  154
                                                                                                                                            91
                                                                                                                                                                         18;
                                                                                                                                                                                       Similarity
                                                                                                                                      GGGAGAATGTAATCATTC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 450; 266pp + Sequence Listing; English.
                                                                                                                  GGGAGAATGTAATCATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Хu J,
                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chenault RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA; 541
                                            CDNA; 2405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                       14.5%;
                                                                                                                                                                         0;
                                                                                                                                                                                       Score 18;
Pred. No.
                                            ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Meagher MJ,
                                                                                                                                                                            Mismatches
                                                                                                                                                                                        DB 24;
. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                450.
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                                                                                                                                                                            0
                                                                                                                                                                                                    Length 541;
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RESULT 41
AAQ92962/
ID AAQ9
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41

AAQ92962 standard; DNA; 2405

ВP

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                                                                                                                                                          This sequence encodes a protein kinase which is an HRR25-like protein. Host cells stably transformed with the protein kinase CC encoding DNA may be used for the expression of the protein kinase such that the expressed protein is "displayed" on the host cell color for antibodies. The host cells may also be used for the production CC protein the cell surface or from the culture medium. CC recombinant HRR25 like proteins display a number of properties which CC recombinant HRR25 like proteins display a number of properties which CC recombination for the protein tryrosine kinases e.g. the HRR25 operates to protein possesses both protein-tryrosine kinase and CC protein serihe/threonine kinase activities. Also, HRR25 operates to composite repair of DNA strand breaks at a specific nucleotide sequence CC protein serihe/threonine kinase activities. Also, HRR25 operates to composite the only protein kinases known to have such CC proteins and host cells expressing them are useful in screening compositions on CC methods designed to examine the effects of various compositions on CC may be a composition of CC proteins are casein kinase activities of the protein. The CC proteins are casein kinase class I protein kinases.

CC Updated on 25-MAR-2003 to correct PN field.)
                                                                                 Best
                                                               Matches
                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein kinase; immunogen; antibody; protein-tyrosine kinase;
protein-serine/threonine kinase; recombination; repair; scree
detection; casein kinase; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wild-type and mutant protein kinase genes and encoded polypeptide(s) - Useful in screening for compositions which effect DNA double strand break repair activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
17-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein kinase (CKIgammalHu) coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 10; Page 97-99; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1994-264102/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JAN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-AUG-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9417189-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                 Sequence 2405 BP; 849 A; 392 C; 486 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAR56529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hoekstra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SALK ) SALK INST BIOLOGICAL STUDIES
                                                               Local Similarity
les 18; Conserv
                               GGGAGAATGTAATCATTC 108
 GGGAGATGTAATCATTC 2224
                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93US-0008001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94WO-US00795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 67..1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= Protein kinase
                                                                               100.0%;
                                                                                 14.5%; Score 18;
100.0%; Pred. No.
                                                                   0;
                                                                   Mismatches
                                                                                                                                    678 T; 0
                                                                                                     DB 15;
                                                                     0;
                                                                                                     Length 2405;
                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                may
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                                                                      Gaps
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RESULT 42
AAH33733/c
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                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                       This human casein-kinase-I (CKI-gamma-1Hu) gene which is a homolog of a DNA recombination and repair gene called HRR25 (HO and/or radiation repair) possesses both protein-tyrosine-kinase and protein serine/tyrosine-kinase activities. HRR25 operates to promote repair of DNA strand breaks at a specific nucleotide sequence and is the only protein-kinase known to have such recombination/repair promoting activity. DNA encoding HRR25 can be used to isolate and identify related sequences, while recombinant HRR25, or cells expressing it, can be used to screen compounds for their effects
                      Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma; ss.
                                                             Human colon
                                                                                                                                                                                                                                                                                                     Sequence 2405 BP; 849 A; 392 C; 486 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New monoclonal antibodies against human casein Kinase class I enzymes - useful for purifon. and determn. of these enzymes and modulate their receptor -ligand binding, also new hybridomas
Homo sapiens
                                                                                      03-SEP-2001
                                                                                                                                      AAH33733 standard; cDNA; 2630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 100; 125pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Casein-kinase-I; HRR25; protein-tyrosine-kinase; CK1-gamma-1HU, protein-serine/threonine-kinase; enzyme; DNA repair;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9519993-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA recombination; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SALK ) SALK INST BIOLOGICAL STUDIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human HRR25-like casein-kinase-I CK1-gamma-1Hu gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ92962;
                                                                                                                                                                                                       2241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1995-269419/35.
DB; AAR76625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens
                                                                                                                                                                                                                              91
                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                               repair
                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                    GGGAGAATGTAATCATTC 2224
                                                                                                                                                                                                                   GGGAGAATGTAATCATTC 108
                                                          cancer antigen
                                                                                                                                                                                                                                                       Conservative
                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                               and kinase activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94US-0185359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95WO-US00955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers 67..1197
                                                                                                                                                                                                                                                                14.5%; Score 18; 100.0%; Pred. No.
                                                          encoding cDNA SEQ ID NO:789
                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                     678 T; 0 other;
                                                                                                                                                                                                                                                                 DB 16;
11;
                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                           Length 2405;
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RESULT 43
AAS84630/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2630 BP; 882 A; 416 C; 435 G; 891 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletion in a patient's genome that affect the activity of P by expressing the protein of the activity of P by expressing the protein of the activity of P by expressing the protein of the activity of P by expressing the protein of the pro
30-MAR-2001; 2001WO-US08631.
                                                      11-OCT-2001.
                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                        DNA encoding novel human diagnostic protein #20434.
                                                                                                                                                                                                                                                                                                                                            13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                AAS84630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS84630 standard; cDNA; 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 2758; 9803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding 4277 human useful for preventing, diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful for preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-SEP-2000; 2000WO-US26524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGAGAATGTAATCATTC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGAGAATGTAATCATTC 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                            (first entry)
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99US-0163280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      colon cancer-associated polypeptides,
and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
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Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Colymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating clisorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity amid to produce other types of data and products dependent on DNA and cliagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the print of the prin
04-FEB-2000; 2000US-0180312
                                              30-JAN-2001; 2001WO-US00662
                                                                                            09-AUG-2001.
                                                                                                                                      WO200157271-A2
                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                          Human; microarray; single exon probe;
                                                                                                                                                                                                                                                                                             Human breast
                                                                                                                                                                                                                                                                                                                                         01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                     ABA46329
                                                                                                                                                                                                                                                                                                                                                                                                                          ABA46329 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 239 BP; 47 A; 87 C; 58 G; 47 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID No 20434; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 CCATCTGCAGGGTCCAG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                            cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCATCTGCAGGGTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                    cell single exon nucleic acid probe #5024
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                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                            88
                                                                                                                                                                                                                                                                                                                                                                                                                             DNA; 355 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                          gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 23; Length 239; 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
 04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      agents on cells. The microarray of this invention presents a far great diversity of probes for measuring gene expression, with far less bit than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                               30-JAN-2001; 2001WO-US00662.
                                                                                                                                                           Homo sapiens
                                                                                                                                                                                         disease; cancer;
                                                                                                09-AUG-2001
                                                                                                                             WO200157271-A2
                                                                                                                                                                                                       Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                        Human breast cell single exon nucleic acid probe #10126
                                                                                                                                                                                                                                                                         01-FEB-2002
                                                                                                                                                                                                                                                                                                                                       ABA51431 standard; DNA; 355 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 5024; 327pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-496933/54.
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04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                      281
                                                                                                                                                                                                                                                                                                                                                                                                                                        22 GGTCCAGGTGATGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULAR DYNAMICS INC
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; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
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2000US-0608408.

2000US-06323687.

2000US-0234687.

2000US-0234687.

2000US-0234687.

2000US-0236359.

2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                            88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.7%;
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Pred. No.
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Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition analysis is useful for prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this pattent did not form part of the printed specification, but was obtained in electronic format directly
04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                         Human foetal liver single exon nucleic acid probe #5194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from humar
                                                                                                                                                WO200157277-A2
                                                                                                                                                                                                  Human;
                                                                                                                                                                                                                                                         01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid probes for measuring gene expression in a sample deri-
from human breast and BT 474 cells. The method involves contacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                          30-JAN-2001;
                                                                                                                      09-AUG-2001
                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                            ABA56889
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                                                                                                                                                                                                    foetal liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comprises number of single exon nucleic acid probes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 10126; 327pp + sequence listing; English
                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                            GGTCCAGGTGATGGATG 297
                                                                                                                                                                                                                                                                                                                                                                                                 GGTCCAGGTGATGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at
         ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
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; 2000US-0234687.
; 2000US-0236359.
; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                           2001WO-US00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP; 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                      (first
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100.0%; Pr
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; 109 G;
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Pred. No.
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39;
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RESULT 47
ABA69454
ID ABA69
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27-SEP-2000;
04-OCT-2000;
                                                                                                                                           26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                          Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
        Claim
                                                                                                                                                                       04-FEB-2000; 2000US-0180312
                                                                                                                                                                                                                                                                       Human; foetal
                                                                                                                                                                                                                                                                                                              01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent printed specification, but was obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a single exon nucleic acid probe for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                         analyzing
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                                                                                                                                                                                                               09-AUG-2001
                                                                                                                                                                                                                                 WO200157277-A2
                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                          Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genome-derived single exon nucleic acid probes useful for
zing gene expression in human fetal liver -
                                   genome-derived
                                                                                                                                                                                                                                                                                         foetal liver single exon nucleic acid probe #17759.
                                                                                                                                                                                                                                                                                                                                                                                                               22 GGTCCAGGTGATGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                         17;
                                                                                            MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ
                                                                                                                                                                                                                                                                                                                                                                                                    GGTCCAGGTGATGGATG
                          gene
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        IJ
                                                                                                                                                    2000US-0207456
2000US-0608408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 122 A; 47 C; 109 G; 77 T; 0 other;
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                                                                                                                        2000US-0234687
2000US-0236359
                                                                                                                                            2000US-0632366
                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences.
                                                                                                               2000GB-0024263
                                                                                                                                                                                                                                                                      liver; gene expression; single exon nucleic acid probe;
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        17759;
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                                   single exon nucleic
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       sequence listing;
                           fetal
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                           acid probes
liver -
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                                   useful
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                                    for
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Matches
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26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-023359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probe of the invention.

Note: The sequence data for this patent did not form part of printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                            Single
hearts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 355 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid
                                    measuring human gene expression in a sample derived from human heart present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derifrom the human heart via microarrays. By measuring gene expression, probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular seg. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    congenital heart disease; ss.
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                                                                                                                                                                Claim 1; SEQ
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  Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200157274-A2
                          congenital heart disease
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17; Conser
                                                                                                                                                                                                        exon
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                                                                                                                                      invention relates to single exon nucleic acid probes for
                                                                                                                                                                                                         nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                            2001WO-US00666
                                                                                                                                                                 ID No
                                                                                                                                                                                                                                                                                                                   2000GB-0024263.
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                                                                                                                                                                4974; 530pp;
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Pred. No.
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39;
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                                                                                             expression in samples derived
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                                                                                                                          from human heart.
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RESULT 49
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                                                                The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    at
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Sequence
                                                                                                                                                                                                           Single exon nucleic acid
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04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABA36383;
                                specification,
                                                          congenital heart disease.
                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                            21-SEP-2000;
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                       scification, but was obtained in electroni
ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                          SG,
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                                   The sequence data for this patent did not form part of the printed fication, but was obtained in electronic format directly from WIPO
                                                                                                                                                                         4;
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2000US-0234687.
2000US-0236359.
2000US-0024263.
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2000US-0608408.
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122
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 109
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Conservative

100.0%; 13.7%;

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No.

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Length 355;

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Mismatches

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Gaps

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Query Match

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RESULT 50
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                                                                                                                 Query Match 13.7%; Score 17; DB 22; Length 355; Best Local Similarity 100.0%; Pred. No. 39; Matches 17; Conservative 0; Mismatches 0; Indels
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26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-0236359.

04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                        The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system, diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                            Single exon nucleic acid probes for analyzing gene expression in human brains - \,
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                                                                                                                                                                            Sequence 355 BP; 122 A; 47 C; 109 G; 77 T; 0 other;
                                                                                                                                                                                                                                                                                                                            Example 4; SEQ ID NO: 4981; 650pp + Sequence Listing; English.
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
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US-09-139-802-200
US-09-659-786-200
US-09-149-476-39
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PCT-US94-14073-1
US-08-652-971-1
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1597, Ap
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28-61/c 13. Application 15. Application 16583108 1NFORMATION: 1NFORMATION: 1NFORMATION: 2AVER COR ANT: DAVIS, 2AVER COR ANT: MILLER, 2D INVENTION: 0F SEQUENCES: 2DONDENCE ADDRES: 2SSEE: MCDONNE 2SSEE: MCDONE 2SSEE: MCDONNE 2SSEE: M	15 12.1 1292 15 12.1 1314 15 12.1 1368 15 12.1 1368 15 12.1 1368 15 12.1 1368 15 12.1 1368 15 12.1 1426 15 12.1 1426 15 12.1 1506 15 12.1 1506 15 12.1 1506 15 12.1 1794 15 12.1 1794 15 12.1 1794 15 12.1 1794 15 12.1 2308 15 12.1 2308
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	Sequence 189, App Sequence 2, Appli Sequence 79, Appl Sequence 79, Appl Sequence 79, Appl Sequence 79, Appli Sequence 79, Appli Sequence 3, Appli Sequence 3, Appli Sequence 4, Appli Sequence 4, Appli Sequence 6, Appli Sequence 11780, Appli Sequence 9, Appli

TELEPHONE: (312) 913-0001 TELEFAX: (312) 913-0002 INFORMATION FOR SEQ ID NO: 61

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; NAME/KEY:
; LOCATION:
US-08-454-097-30
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                                                                                                                                                                                                                                                                                   PILING DATE: 21-JAN-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,783

FILING DATE: 03-JUL-1991

ATTORNEY/AGENT INFORMATION:
NAME: NO. 5686412and, Greta E.
REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27866/3185:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                        TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 2405 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185,359
FILLING DATE: 21-JAN-1994
APPLICATION NUMBER: US 08/008,001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hoekstra
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                Local Similarity
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TELEPHONE: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                              TOPOLOGY:
                                                                                                                                                        STRANDEDNESS: single
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233 South Wacker Drive,
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100.0%; Pred. No.
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               14.5%; Score 18; DB 1; 100.0%; Pred. No. 1.8;
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cker Drive, 6300 Sears Tower
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                              Length 2405;
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US-09-328-352-1220
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US-08-185-359-30/c
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GENERAL INFORMATION:
APPLICANT: GARY L. Breton et al.
APPLICANT: GARY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
                                                                                   Sequence 1220, Application US/09328352
Patent No. 6562958
                                                                                                                                                                                                                                                          Matches
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APPLICANT: Hoekst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/008,001
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,783
FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: NO. 6060296and, Greta
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27/
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polon-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 312-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 312-474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Chicago
STATE: Illinois
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o. 6060296 ·
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18; Conserv
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100.0%; Pred. No. 1.8;
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GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
APPLICANT: Rasqualini, Renata
TITLE OF INVENTION: NGR Receptor and Method
TITLE OF INVENTION: Molecules That Home to
TITLE OF INVENTION: Same
FILE REFERENCE: P-LJ 3203
CURRENT APPLICATION NUMBER: US/09/659,786
CURRENT FILING DATE: 2000-09-11
PRIOR APPLICATION NUMBER: 08/926,914
PRIOR APPLICATION NUMBER: 08/926,914
PRIOR FILING DATE: 1997-09-10
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Best Local Similarity
Marches 17; Conserve
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; ORGANISM: Acinetobacter baumannii
US-09-328-352-1220
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CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1220
LENGTH: 363
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Best Local (
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LENGTH: 3494
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Patent No. 6180084
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APPLICANT: Rudslahti, Renata
TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
TITLE OF INVENTION: Same
TILE REFERENCE: P-LJ 3203
CURRENT APPLICATION NUMBER: US/09/139,802
CURRENT FILING DATE: 1998-08-25
EARLIER APPLICATION NUMBER: 08/926,914
EARLIER APPLICATION NUMBER: 08/926,914
EARLIER FILING DATE: 1997-09-10
EARLIER FILING DATE: 1996-09-10
PRIOR APPLICATION NUMBER: 08/
PRIOR FILING DATE: 1996-09-10
NUMBER OF SEQ ID NOS: 226
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NAME/KEY: CDS
LOCATION: (121)...(3024)
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17; Conserv
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, 100.0%; Pr
                                                                                                                                                                                         Molecules That Home to Angiogenic Vasculature Using
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; LOCATION: (121)..(3024)
US-09-659-786-200
                                                                                                            US-08-961-527-98
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                                                      Matches
                                                                Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                                                           TELEFAX: (301) 309-851:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION UNMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5;
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS VE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Charles I
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 9410 Key
CITY: Rockville
                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                        TELEPHONE:
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                                                                                                                                                                  LENGTH:
1105
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                 74 GACTGTGTTGTGGTCTG 90
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GACTGTGTTGTGGTCTG 1089
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                                                      Conservative
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100.0%; Pr
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                                                                13.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.50 inch, 1.4Mb storage
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                                                                   Score 17; ; Pred. No.
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                                                                   DB 4;
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6.1;
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RESULT 8 US-09-313-294A-3641/c ; Sequence 3641, Application US/09313294A

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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte II
; NAME/KEY: unsure
; LOCATION: 128
; OTHER INFORMATION: a, t, c,
US-09-313-294A-3641
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SEQ ID NO 3641
LENGTH: 266
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GENERAL INF
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Best Local
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APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES
FILE REFERENCE: PL-0017 US
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EARLIER
EARLIER
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EARLIER
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CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rosen et al. TITLE OF INVENTION: 186 Human Secreted proteins FILE REFERENCE: PZ002P1
                                                                                           EARLIER
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lo. 6420526
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                                                                         APPLICATION NUMBER: 60/047,502
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,633
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FILING DATE: 1997-03-07
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                                          APPLICATION NUMBER: 60/047,583
                                                                                                                       APPLICATION NUMBER: 60/047,597 FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/038,621
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APPLICATION NUMBER: 60/047,615
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APPLICATION NUMBER: 60/056,877
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APPLICATION NUMBER: 60/047,613
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                                 FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/056,880
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,903
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                                                                                  60/056,909
                                                                                                                                                                                 60/056,664
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FILE REFERENCE: PZ00ZP1

CURRENT APPLICATION NUMBER: US/09/149,476

CURRENT FILING DATE: 1998-09-08

EARLIER APPLICATION NUMBER: 60/040,162

EARLIER APPLICATION NUMBER: 60/040,162

EARLIER APPLICATION NUMBER: 60/040,333

EARLIER FILING DATE: 1997-03-07

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,626

EARLIER APPLICATION NUMBER: 60/040,626

EARLIER APPLICATION NUMBER: 60/040,626

EARLIER APPLICATION NUMBER: 60/040,626

EARLIER APPLICATION NUMBER: 60/040,334

EARLIER APPLICATION NUMBER: 60/040,334

EARLIER APPLICATION NUMBER: 60/040,334

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,606

EARLIER APPLICATION NUMBER: 60/047,600

EARLIER APPLICATION NUMBER: 60/047,600

EARLIER APPLICATION NUMBER: 60/047,615

EARLIER APPLICATION NUMBER: 60/047,597

EARLIER APPLICATION NUMBER: 60/047,597

EARLIER APPLICATION NUMBER: 60/047,597

EARLIER APPLICATION NUMBER: 60/047,633

EARLIER APPLICATION NUMBER: 60/047,533

EARLIER APPLICATION NUMBER: 60/047,618

EARLIER APPLICATION NUMBER: 60/047,618

EARLIER APPLICATION NUMBER: 60/047,503

EARLIER APPLICATION NUMBER: 60/047,503
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US-09-149-476-76/c
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Best Local S
Matches 16
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER
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ER APPLICATION NUMBER: 60/056,908
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/048,964
ER FILING DATE: 1997-06-06
ER FILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/057,650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R FILING DATE: 1997-09-05
R APPLICATION NUMBER: 60/08
R FILING DATE: 1997-06-13
R FILING DATE: 1997-10-02
R FILING DATE:
R APPLICATION N
R FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 TCTGCAGGGTCCAGGT 30
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100.0%; Pred. No. 21
cive 0; Mismatches
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ER APPLICATION NUMBER: 60/047,598
ER FILLING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,613
ER FILLING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,582
ER FILLING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,596
ER APPLICATION NUMBER: 60/047,612
ER APPLICATION NUMBER: 60/047,612
ER APPLICATION NUMBER: 60/047,612
ER FILLING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,612
ER FILLING DATE: 1997-05-23

APPLICATION NUMBER: 60/047,601 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,580 FILING DATE: 1997-04-11

APPLICATION NUMBER: 60/047,632 FILING DATE: 1997-05-23

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APPLICATION NUMBER: 60/047,587 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,492 FILING DATE: 1997-05-23

APPLICATION NUMBER: 60/047,584 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,500 FILING DATE: 1997-05-23

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,875 ,862 ,887 ,908 ,908	57 57 57 57 57 57 57 57 57 57	,892 ,595 ,595 ,588 ,586 ,586 ,589 ,589	,880 ,894 ,911 ,636 ,874 ,910 ,864 ,845

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ER APPLICATION NUMBER: 60/043,568
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,314
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,569
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,311
ER APPLICATION NUMBER: 60/043,671
ER APPLICATION NUMBER: 60/043,671
ER FILING DATE: 1997-04-11
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,674
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,669
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,669
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,313
ER FILING DATE: 1997-04-11

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ER APPLICATION NUMBER: 60/043,672
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,315
ER FILING DATE: 1997-06-06
ER APPLICATION NUMBER: 60/056,886
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,893
ER APPLICATION NUMBER: 60/056,893
ER APPLICATION NUMBER: 60/056,893
ER APPLICATION NUMBER: 60/056,893
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,630
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,630
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,630
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,662
ER APPLICATION NUMBER: 60/056,662
ER APPLICATION NUMBER: 60/056,873
ER APPLICATION NUMBER: 60/056,872
ER APPLICATION NUMBER: 60/056,872
ER APPLICATION NUMBER: 60/056,872
ER APPLICATION NUMBER: 60/056,872
ER APPLICATION NUMBER: 60/056,882
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,882
ER FILING DATE: 1997-08-23
ER APPLICATION NUMBER: 60/056,882
ER APPLICATION NUMBER: 60/056,883
ER FILING DATE: 1997-08-23
ER APPLICATION NUMBER: 60/056,883

APPLICATION NUMBER: 60/056,884

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                                                                    ; LOCATION:
US-08-163-919A-1
                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IPC-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 1:
Query Match 12.9
Best Local Similarity 100
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08163919A Patent No. 6180771
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Best Local
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                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/01
FILING DATE: 08-DEC-1993:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/163,919A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
                                                                                                     FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: THOMAS, Wayne R., CHUA, Kaw-Yan, ROGERS, Bruce L., APPLICANT: KUO, Mei-chang
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING A HOUSE DUST MITE
TITLE OF INVENTION: ALLERGEN, DER P III, AND USES THEREFOR
                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                      LENGTH: 1059 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
                                                                                                                                       LOCATION:
                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
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FILING DATE: 1997-06-13
APPLICATION NUMBER: 60/061,060
FILING DATE: 1997-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/057,669
FILING DATE: 1997-09-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 State Street suite 510
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150..848
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                                                                                                                                     63..848
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                 12.9%; Score 16; DB 3; 100.0%; Pred. No. 21;
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100.0%; Pred. No. 21
tive 0; Mismatches
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   0
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   Mismatches
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 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                   Length 1059;
   Indels
 0;
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RESULT 13
US-08-652-971-1/c
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                                                                                                                                                                                                                                                                                                                    PCT-US94-14073-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US94-14073-1
                                                                   Sequence 1, Application US/08652971 Patent No. 5814507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application:
                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                               Best Local Similarity 100.0%;
GENERAL INFORMATION:
APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laur
TITLE OF INVENTION: A )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII TEXT
CURRINT APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 08-DEC-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UMBER:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IPC-072 (IMI-041)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
COMPUTER: IBM PC componenting System: PC
OPERATING SYSTEM: PC
                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
STREET: 60 State Street suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: THOMAS, Wayne R., CHUA, Kaw-Yan, ROGERS, Bruce L., APPLICANT: KUO, Mei-chang
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING A HOUSE DUST MITE
TITLE OF INVENTION: ALLERGEN, DER P III, AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1059 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                                                                                                                                                               958
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                                                                                                                                                                                                                                                                                                                                                                                       CDS
63..848
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                  mat_peptide
150..848
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                    Laurence A.
                                                                                                                                                                                                                                                                               12.9%;
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                                                                                                                                                                                                                                                                 Score 16; Pred. No.
                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                               Length 1059;
                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                              Gaps
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A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE

NUMBER OF SEQUENCES:

FITLE OF INVENTION:

PHOSPHATASE, PTP LAMBDA

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RESULT 14
US-08-991-258A-1/c
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5928887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEY: (415) 952-9881
TELEX: 910 371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 3,055
REFERENCE/DOCKET NUMBER: P103
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 225-3216
TELEFAX: (415) 952-9881
                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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LOCATION:
                                                                                                                                                                                              CITY: San Francisco
STATE: California
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd.
CITY: South San Francisco
                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                              ADDRESSEE:
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 CLASSIFICATION:
                                 APPLICATION NUMBER:
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                                                                                                                                                                             United States
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17-DEC-1997
: 435
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                                 US/08/991,258A
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US-08-769-399-1/c
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                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 91,055
REFERENCE/DOCKET NUMBER: P103:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 225-3216
TELEPAX: (415) 952-9881
TELERAX: 910 371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TENTORUS CTO base mairs
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REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-63
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
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                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cheng, Jili
APPLICANT: Lasky, Laurence A.
APPLICANT: Lasky, Laurence A.
A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 24-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd.
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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   MOLECULE TYPE:
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LOCATION:
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                                 STRANDEDNESS:
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5. 5976852
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                              nucleic acid
DEDNESS: single
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379..4686
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DNA (genomic)
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                                                                      Query Match
Best Local Similarity
                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08991953A Patent No. 6083748
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 00 FILING DATE: 24-MAY-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/652,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                              FEATURE:
                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                               NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 16-DEC-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                            TELEFAX:
                                                                                                                                                                                                    STRANDEDNESS: single
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Trerecretededada 875
                           TTGTGGTCTGGGGAGA 96
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                                                                                                                                                                                                                                                                                           (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States
                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.30
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379..4686
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379..4686
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100.0%; Pr
                                                                    12.9%; Score 16;
100.0%; Pred. No.
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; Pred. No.
                                                        Mismatches
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21;
                                                                       DB 3;
21;
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                                                                                  Length 5769;
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RESULT 17

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RESULT 18
US-09-313-294A-2588/c
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                                                                         GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
APPLICANT: SNERMAN, BRADLEY N.
TITLE OF INVENTION: POLYNUCLEO
                                                                                                                                                                    Sequence 2588, Application US/09313294A Patent No. 6476212
                                                                                                                                                                                                                                                                                                                                  Matches
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FILE REFERENCE: PL-0017 US CURRENT APPLICATION NUMBER: US/09/313,294A

RUMBER OF SEQ ID NOS: 7600
                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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APPLICANT: NISHIZ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: WO PCT
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 93/
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,76
                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOPFWADER. BASSAFT PS-TOSTON
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/663,08
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Anabaena variabilis
STRAIN: IAM M-3
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3000 K Street, N.W., Suite 500
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GENE FOR FATTY ACID DESATURASE, VECTOR
CONTAINING SAID GENE, PLANT TRANSFORMED WITH SAID GENE,
AND PROCESS FOR CREATING SAID PLANT
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RESULT 19
US-08-309-182B-2
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                                                           US-08-309-182B-2
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               Query Match
Best Local S
   Matches
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OTHER INFORMATION: Incyte ID No. 6476212 700552942H1
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SEQUENCE CHARACTERISTICS:
LENGTH: 819 base pairs
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                                                                                                                                                                                                                                                                                                     NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367 REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: September CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth,
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                                                                                                                                              MOLECULE TYPE:
ORIGINAL SOURCE:
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                                                                                                                   FEATURE:
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                                                                                      NAME/KEY:
LOCATION:
y Match 12.1%; So
Local Similarity 100.0%; I
hes 15; Conservative 0;
                                                                                                                                ORGANISM:
                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                         TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/
FILING DATE: September 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
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                                                                          IDENTIFICATION METHOD:
                                                                                                                                                                            TOPOLOGY:
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805 Fifteenth Street, N.W., #700
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                                                                                                                                Anabaena variabilis
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100.0%;
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   Score 15; DB 1; ; Pred. No. 71; 0; Mismatches
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                               Length 819;
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RESULT 22
US-09-252-991A-5529/c
; Sequence 5529, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11595
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PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 11847
LEEGTH: 942
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LENGTH: 978
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APPLICANT: Marc J.
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Best Local Similarity
Matches 15; Conserv
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CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
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TITLE OF INVENTION: NUCCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa
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15; Conserv
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Pred. No.
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71;
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GENERAL INFORMATION:

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-0
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                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: unsure
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                                                                                                      REFERENCE/DOCKET NUMBER: IM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                           FILING DATE: August 15, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17, 1989
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                              FILING DATE: March 17, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rogers, Bruce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                ENGTH:
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VENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
VENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
              1196 base pairs
ucleic acid
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                                                                    (617)227-5941
(7) 70 NO: 71:
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State Street, suite 510
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1998-02-18
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100.0%; Pred. No.
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                                                                                             Query Match
Best Local 9
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                                                                   Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PILING DATE: August 15, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Are a Mandataneous and the second seco
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617)227-5941
[NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,448A
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                                                                                                                                                                                                                                                                                   FEATURE:
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                                                            Local Similarity
les 15; Conserv
                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 1...
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                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
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      AGAATGTAATCATTC 108
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Rafnar, Thorunn
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100.0%; Pr
                                                                                         12.1%; Score 15; 100.0%; Pred. No.
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Pred. No.
                                                                   Mismatches
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                                                        Patent No. 6335019
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David
APPLICANT: Rafnar, Thoru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-175-069A-71
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Best Local S
Matches 15
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
1106 hase pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: IM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                  TITLE OF INVENTION:
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APPLICATION NUMBER: US/08/175,069A
FILING DATE: December 29, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: March 17, 198
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,20
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PRIOR APPLICATION NUMBER: US 07/529,951
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ADDRESSEE: LAHIVE & COCKFIELD, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1196 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/529,951 FILING DATE: May 29, 1990 APPLICATION NUMBER: US 07/325,365 FILING DATE: March 17, 1989
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
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                                                                   Klapper, David (Rafnar, Thorunn
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Rafnar, Thorunn
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                                               Kuo, Mei-chang
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Methods For Treating Sensitivity To A
Protein Allergen Using Peptides Which Inlcude A T Cell
93
                                                                                                                                                                                                                                                                                                                                12.1%; Score 15; DB 1; 100.0%; Pred. No. 71;
                                                                                   David G.
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Best Local :
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APPLICANT: I
APPLICANT: I
APPLICANT: I
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                         NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/464,000
FILING DATE: 05-TUN-1995
APPLICATION NUMBER: US 08/290,448
FILING DATE: 15-AUG-1994
APPLICATION NUMBER: US 07/529,951
FILING DATE: 29-MAY-1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: 17-MAR-1989
                                                                                                                                                                                        APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Peptides from Ragweed Pollen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: cDNA FEATURE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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05-JUN-1995
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100.0%; Pred. No.
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RESULT 28
US-09-205-258-189
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                               CURRENT
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TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
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APPLICATION NUMBER: US 07/529,951
FILING DATE: 29-MAX-1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: 17-MAR-1989
ATTORNEY/AGENT INFORMATION:
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LENGTH: 1196 base pairs
TYPE: nucleic acid
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APPLICATION NUMBER: 1
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REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018CN2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/01
FILING DATE: 05-JUN-1995
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o. 65251
                                                                                                                           FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/049,020
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,876
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,881
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,885
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,895
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,884
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APPLICATION NUMBER: 60/048,896
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               APPLICATION NUMBER: 60/048,894 FILING DATE: 1997-06-06
                                             FILING DATE:
                                                                                                                                                                                                                              APPLICATION NUMBER: 60/048,880
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(617)227-5941
OR SEQ ID NO: 71:
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; ORGANISM: Homo sapiens
US-09-205-258-189
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EARLIER FILING DATE: 1997-06-
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EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
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FILING DATE: 1997-06-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/048,917
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57 CTGAAAACAAACAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILING DATE: 1997-06-06
                                                                                      Similarity
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                                                        12.1%; Score 15; DB llarity 100.0%; Pred. No. 71 Conservative 0; Mismatches
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RESULT 29 US-09-025-059-2

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RESULT 30
US-08-290-448A-79
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Best Local (
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GENERAL INFORMATION:
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                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                    APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic
NUMBER OF SEQUENCES: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                           APPLICANT:
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                                          CORRESPONDENCE ADDRESS:
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APPLICANT: Guegler, Karl J.
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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LIBRARY: 2723646
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                         ADDRESSEE:
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SOFTWARE: FastSE(
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             STREET:
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Boston
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                                                                                                                                                                        Application US/08290448A
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          E: LAHIVE & COCKFIELD 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1314 base pairs
                                                                                             Klapper, David (Rafnar, Thorunn
                                                                                                                          Rogers, Bruce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        650-845-4166
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                                                                                                                 David G.
                                                                                                                                                                                                                                                                                                                   12.1%; Score 15; 100.0%; Pred. No.
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                                                                   Proteins From Ragweed and Uses
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US-08-290-448A-79
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                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
NAME: Amy E. Mandragouras
FILING DATE: August 15, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: August 15
                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 11:
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TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                       IITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                        CITY: Boston
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5. 5698204
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EDNESS: single
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Rafnar, Thorunn
                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                        Mei-chang
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                                                                                                                                                                                                                                                                                                                                                                         David G.
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                                                                  US/08/290,448A
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Pred. No.
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ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandradon

Mandragouras

APPLICATION NUMBER:

US 07/325,365

1989

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Best Local
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                                                                                                              PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/529,951

FILING DATE: May 29, 1990

APPLICATION NUMBER: US 07/325,365

FILING DATE: March 17, 1989

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: IMI-018DV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                            TELEFAX: (617)227-594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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      LENGTH:
                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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STRANDEDNESS: single
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REFERENCE/DOCKET NUMBER: IMI-018CN
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1368 base pairs
ucleic acid
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                                                                (617)227-5941
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US-08-461-939B-79
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Best Local Similarity
                                                                                                                                                          TELEPHONE: (617)227-7
TELEFAX: (617)742-421
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                   FEATURE:
                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IM
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 05-JUN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Methods For Treating Sensitivity To A
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                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/290,448
FILING DATE: 15-AUG-1994
APPLICATION NUMBER: US 07/529,951
FILING DATE: 29-MAY-1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: 17-MAR-1989
                                NAME/KEY: CDS
                                                                                        LENGTH: 1368 base pairs
TYPE: nucleic acid
STRANGENESS: single
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                                                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 State Street
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Query Match Best Local Similarity

Score 15; Pred. No.

DB 4; 71;

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RESULT 34
US-08-464-000-79
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US-09-121-425-3
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Best Local S
Matches 15
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           Sequence 3, Application US/09121425
Patent No. 6153418
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GENERAL
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                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617)227-5941 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Peptides from Ragweed Pollen
NUMBER OF SEQUENCES: 93
                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018CN2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1368 base pair
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 29-MAY-1990
APPLICATION NUMBER: US 07
FILING DATE: 17-MAR-1989
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                              MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Palana
                                                                                                                                                                                                                                                  NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Amy E. Mandragouras REGISTRATION NUMBER: 36,2
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INFORMATION:
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                                                                                                                                     94 AGAATGTAATCATTC 108
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                                                                                                                                                                                     Similarity
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                                                                                               AGAATGTAATCATTC 466
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                                                                                                                                                                                   Score 15;
Pred. No.
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71;
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US-08-149-105-4/c
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Best Local S
Matches 15
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LENGTH: 1426
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                                                                                                                        Sequence 4, Application US/08149105 Patent No. 5538892
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CURRENT APPLICATION NUMBER: US/09/634,493A
CURRENT FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: US/09/121,425
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 20
                                                                           GENERAL INFORMATION:
APPLICANT: Donaho
APPLICANT: Gustafi
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CURRENT FILING DATE: 1998-07-23
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TITLE OF INVENTION: Consensus Phytases
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TITLE OF INVENTION: Consensus Phytases
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                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                  APPLICANT: Wang, Xiao-Fan TITLE OF INVENTION: TGF-NUMBER OF SEQUENCES: 17
                                                 APPLICANT:
 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                   Local Similarity nes 15; Conserv
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                                                                He, Wei W.
                                                                             Gustafson,
                                                                                             Donahoe, Patricia K.
                                                                                                                                                                                                                                                                                    Conservative
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                                                                               Michael
                                    TYPE I RECEPTOR
                                                                                                                                                                                                                                                                                                   Score 15;
; Pred. No.
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ADDRESSEE: STREET: 2:

225 Franklin Street

Fish & Richardson

02110-2804

U.S.A

Massachusetts

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Best Local S
Matches 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/029,67
FILING DATE: March 11, 1993
APPLICATION NUMBER: 07/853,39
FILING DATE: March 18, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
PREFERENCE/DOCUMENT: NAME: 0770
                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM 92 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Donahoe, Patricia K.
APPLICANT: Gustafson, Michael
APPLICANT: He, Wei W.
TITLE OF INVENTION: FOUR NOVEL
TITLE OF INVENTION: FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.1)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEPAX: (617) 542-8906
PRIOR APPLICATION DATA:
                   FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                           CITY: Boston
STATE: Massac
                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE:
                                                      APPLICATION NUMBER:
                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                   ADDRESSEE:
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02110-2804
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DEDNESS: double
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                                                                                                                                                                                                                                                                225 Franklin Street
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07/853,396
                                                      US/08/317,847
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27.
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US-09-252-991A-5553/c
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                                                                                                                                                                                                              RESULT 40
US-09-252-991A-11780
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILLING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
SEQ ID NO 5553
LENGTH: 1545
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                                                                                                                                                                        Sequence 11780, App. Patent No. 6551795
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/127002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: March 18, 1
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 10.
TELEFAX: 200154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                      1280 TGCGCCATCTGCAGG 1266
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15; Conserv
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VENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
VENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                 Conservative
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UMBER: 07/853,396
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100.0%; Pred. No. 70;
ive 0; Mismatches
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                                                           Best Loc
Matches
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LENGTH: 1605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                TELEFAX: 617 876 5851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1794 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: WOZNEY, John
APPLICANT: CELESTE, Anthony J.
APPLICANT: THIES, R. Scott
APPLICANT: YAMAJI, No. 6291206oru
TITLE OF INVENTION: RECEPTOR PROTEINS
                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 617 876 1170
                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: LAZAR, Steven R
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
                                                                                                                                                                                   IMMEDIATE SOURCE:
CLONE: W-120
                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 8/ Cambridge
                                                           Local Similarity
mes 15; Conserv
                                                                                                                                    NAME/KEY: CDS
LOCATION: 83..1591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                    TOPOLOGY:
                             102 ATCATTCCTTCCACA 116
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ATCATTCCTTCCACA 976
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                                                          12.1%; Score 15; llarity 100.0%; Pred. No. Conservative 0; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics Institute Inc. - Legal Affairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                    DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                         17-SEP-1993
N: 530
                                                                                                                                                                                                                                                 single
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                                                                                                                                                                                                                                                                                                                                                                                         32,618
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                                                             Mismatches
                                                                          DB 3;
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                                                                                          Length 1794;
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US-09-252-991A-5670
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PCT-US94-10080-9/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US94-10080-9
                                                                                                                                                               Sequence 5670, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application PC/TUS9410080 GENERAL INFORMATION:
APPLICANT: GENETICS INSTITUTE, INC.
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 15; Conserv
                                                     APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-0 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617) 876-585
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: LAZAK, Steven R
REGISTRATION UNMER: 32,618
REFERENCE/DOCKET NUMBER: 5203
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8260
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION UMBER: PCT/US94/10080
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
CLONE: W-120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,934
FILING DATE: 17-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
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CITY: Cambridge
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                          990 ATCATTCCTTCCACA 976
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83..1591
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                   .998-02-18
                                 1999-02-18
BER: US 60/074,788
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100.0%; Pred. No.
 US 60/094,190
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1998-07-27

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RESULT 44
US-09-382-256-9/c
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5670
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Best Local S
Matches 15
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GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 5670
LENGTH: 1914
                   INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MIIAGONO, PETER
TEN DIJKE, PETER
FRANZEN, Petra
YAMASHITA, Hidetoshi
HELDIN, Carl-Henrik
TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES, HAVING SERINE THREONINE KINASE
AND THEIR USE
                                                                NAME: No. 6207814man D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5298.1
TELECOMMUNICATION INFORMATION:
                                                                                                                                            FILING DATE: July 2, 1993
APPLICATION NUMBER: 9316099.2
FILING DATE: August 3, 1993
APPLICATION NUMBER: 321344.5
FILING DATE: October 15, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA: NS/09/382,256A
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
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15; Conserv
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                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: GB 9304677.9 FILING DATE: March 8, 1993 APPLICATION NUMBER: GB 9304680.3 FILING DATE: March 8, 1993
                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: No. 6207814ember 17, 1993
APPLICATION NUMBER: GB 9224057.1
FILING DATE: No. 6207814ember 17, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 24-Aug-1999 CLASSIFICATION: 514
                                                    TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PS/2
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                                     TELEFAX:
                                                                                                                                                                                                                                                   PILING DATE: March 8, 1993
APPLICATION NUMBER: 9311047.6
PILING DATE: May 28, 1993
APPLICATION NUMBER: 9313763.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/GB93/02367
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                   FOR SEQ ID NO:
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                                     752-5958
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GENERAL INFORMATION:
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                                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/436,265

FILING DATE: 30-October-1995

APPLICATION NUMBER: PCT/GB93/02367

FILING DATE: 17-No. 6271365ember-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 9224057.1

FILING DATE: 17-No. 6271365ember-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 9304677.9

PRIOR APPLICATION NUMBER: 9304677.9
              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9:
FILING DATE: 28-May-10:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Miyazono, Kohei; Dijke, Peter Ten;
APPLICANT: Franzen, Petra; Yamashita, Hidetos
TITLE OF INVENTION: Activin Receptor-Like Kin
TITLE OF INVENTION: Having Serine Threonine K
                                                                                                               FILING DATE: 8-March-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 93046
FILING DATE: 8-March-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DO
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US.
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ADDRESSEE: Felfe & Lynch
  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York ZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 805 Third Avenue CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 9:
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LOCATION: 77..1585
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                                                           28-May-1993
2-July-1993
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Having Serine Threonine Kinase Domains And Their Use
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                                                                            9311047.6
                                                                                                                                      9304680.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.5 inch, 360 kb storage
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ATTORNEY/AGENT INFORMATION:

APPLICATION NUMBER: 9321344. FILING DATE: 15-October-1993

9321344.5

PRIOR APPLICATION DATA:

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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212) 838-3884
NFORMATION FOR SEQ ID NO:
              FILING DATE: 8-March-1993 PRIOR APPLICATION DATA:
                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02367
FILING DATE: 17-No. 6316217ember-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9224057.1
FILING DATE: 17-No. 6316217ember-1992
                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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NAME/KEY:
                                                        PRIOR APPLICATION DATA:
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ORIGINAL SOURCE:
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LENGTH: 2308 base pair
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TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                  STREET:
                            APPLICATION NUMBER: 9304677.9 FILING DATE: 8-March-1993
                                                                                                                                                          FILING DATE: 30 CLASSIFICATION:
                                                                                                                                                                   APPLICATION NUMBER: US/08/436,265
FILING DATE: 30-October-1995
                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                   STATE:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Kohlei, Vineet
REGISTRATION NUMBER: 37
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mouse
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F: 805 Third Avenue
New York City
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YPE: internal
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                                                                                                                                                                                                                                                      Diskette, 3.5 inch, 360 kb storage
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9304680.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2308;
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                                                                                                                                                                                                                                                                                                                                                                                                              Carl-Henrik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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US-09-679-187-9/c
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                          APPLICANT: Miyazono,
APPLICANT: Franzen, F
TITLE OF INVENTION: F
TITLE OF INVENTION: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
DATE: 30-October-1995
PRIOR APPLICATION DATA:
                                                      APPLICATION NUMBER: US/09/679,187
FILING DATE: 03-0CT-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/436,265
                                                                                                                     OPERATING SYSTEM: PC-DOS SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSES: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 9321:
FILING DATE: 15-October-
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                     CITAL: NC.
STATE: NC.
10022
PEAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Kohlei, Vineet
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 3-Augus PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 9313
FILING DATE: 2-July-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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Local 5.
15;
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APPLICATION NUMBER:
                                                                                                                                                                       COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        984 ATCATTCCTTCCACA 970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 ATCATTCCTTCCACA 116
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Similarity 100.0%; Pred. No.
15; Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
                                                                                                                                                                                                                                 New York
                                                                                                                                                                                                                                                                                                                                                                            Miyazono,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NO
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                                                                                                                                                                                  Diskette, 3.5 inch,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      838-3884
                                                                                                                                                                                                                                                                                                                            Having Serine Threonine Kinase Domains And Their Use
                                                                                                                                                                                                                                                                                                                                           , Kohei; Dijke, Peter Ten;
Petra; Yamashita, Hidetoshi;
Activin Receptor-Like Kinase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9313763.6
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                                                                                                                                                                                  360 kb storage
                                                                                                                                                                                                                                                                                                                                                          Hidetoshi; Heldin, Carl-Henrik
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:

APPLICATION NUMBER: 17-NO

17-No. 6331621ember-1992

9224057.1

FILING DATE:

8-March-1993

9304677.9

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

PCT/GB93/02367 . 6331621ember-1993

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RESULT 48
US-09-489-847-67
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                                                                                                                                                                                         Sequence 67, Application US/09489847
Patent No. 6476195
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
                                                                             EARLIER APPLICATION NUMBER: PCT/US99/17130
EARLIER FILING DATE: 1999-07-29
                                                                                                           CURRENT APPLICATION NUMBER: US/09/489,847 CURRENT FILING DATE: 2000-01-24
                                                                                                                                           APPLICANT: Rosen et al TITLE OF INVENTION: 98 Human Secreted Proteins FILE REFERENCE: PZ031P1
                EARLIER
EARLIER
                                           EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PILING DATE: 3-August-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9321344.5
FILING DATE: 15-October-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kohlei, Vineet
REGISTRATION NUMBER: 37,003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (212) 838-3884
NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2-July-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 28-May-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 93046 FILING DATE: 8-March-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 9136099.2
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                                                                                                                                                                                                                                                                                                           984 ATCATTCCTTCCACA 970
                                                                                                                                                                                                                                                                                                                                        102 ATCATTCCTTCCACA 116
APPLICATION NUMBER: 60/096,319
                APPLICATION NUMBER: 60/095,486 FILING DATE: 1998-08-05
                                                                                                                                                                                                                                                                                                                                                                        1 Similarity 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NO
YPE: internal
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77..1585
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                                                                                                                                                                                                                                                                                                                                                                     12.1%; Score 15;
100.0%; Pred. No.
ative 0; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
70;
                                                                                                                                                                                                                                                                                                                                                                                                      Length 2308;
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; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PATENTIN Ver. 2.0
; SEQ ID NO 67
                                                                                                                                                                                                                                                                                                                 RESULT 49
US-07-959-943-10/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: SITE
; LOCATION: (130)
; OTHER INFORMATION: n equals a,t,9, or
US-09-489-847-67
                                                                                                                                                                                                                                                                                    Sequence 10, Application US/07959943 Patent No. 5418162
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: SITE LOCATION: (73)
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: SITE LOCATION: (103)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: SITE
LOCATION: (75)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: n equals a,t,g,
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EATURE
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                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                              TITLE OF INVENTION: Serotonin Transporter cDNA NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                           APPLICANT: Blakely, Randy D.
APPLICANT: Fremeau Jr., Robe
APPLICANT: Caron, Marc G.
                                                                    CITY: Raleigh
STATE: NO. 5418162th Carolina
COUNTRY: U.S.A.
                                                           COUNTRY: U
ZIP: 27622
                                                                                                                  ADDRESSEE: Gibson
STREET: Post Office Drawer 31107
                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           15;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 100.
15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (27)
                                                                                                                                                                 Kenneth D. Sibley; Bell, Seltzer, Park
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                                                                                                                                                                                                                                          Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a,t,g,
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SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

US/07/959,943

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В
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; LOCATION:
US-07-959-943-10
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US-08-551-459-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 12.1
Best Local Similarity 100
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Huang, Yue
APPLICANT: Karatzas, Costas N.
APPLICANT: Karatzas, Costas N.
APPLICANT: Lazaris-Karatzas, Anthoula
APPLICANT: Delaquis, Annick
TITLE OF INVENTION: ASPERGILLUS NIGER BE
TITLE OF INVENTION: GENE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2508 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   equence 3, Application US/08551459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE DOCKET NUMBER: 540
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: cDNA
POSITION IN GENOME:
UNITS: 2278 basepairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0:
FILING DATE: 19921014
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                    ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06632/005001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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STREET: 22.
STRY: Boston
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TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
                                                                                                                                                                                             CLASSIFICATION: 435
                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/551,459
                                                                                                                                                                                                                                                                                                                                                                                                      STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          737 AGGGTCCAGGTGATG 723
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225 Franklin Street
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73..1962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASPERGILLUS NIGER BETA GALACTOSIDASE
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; MOLECULE TYPE: CDNA
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus niger
US-08-551-459-3
DЬ
                                                 Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                   LENGTH: 3057 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
 248 AGATGTCAAGCTGAA 234
                       47 AGATGTCAAGCTGAA 61
                                                   Conservative
                                                               12.1%; Score 15; DB 1; 100.0%; Pred. No. 70;
                                                      0
                                                       Mismatches
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Gaps

0

Search completed: November 7, 2003, 11:59:34 Job time : 34.5936 secs

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Word size
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Gapop 60.0 , Gapext 60.0
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gb ro:*
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gb sts:*
gb sts:*
gb vi:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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98496 Rattus	06176 Rattu	777	ASAUG HOMO	03666 Mus	96983 SAG:a	2 SAG:a	96973 SAG:a	12226 Homo sa	25667 Rattus	19145 Rattus n	D096993 SAG:a	096984 SAG:	5698 Ratt	18192 Mus n	164679 Homo	005966 Homo	627 Homo s	878 Homo	96995 SAG:	6994 SAG:	D096992 S	D096991 SAG	D096990 SAG:	D096989 SAG	D096988 SAG:	6987 S	96986 SAG	6985 SAG:	96981 SAG:	96967 SAG:ap	07348 Homo	42060 Ho	82592 Sec	77705 5'ES	18192 Mus	03666 Mus	71691	8615 Mus mus	929565 Mous	3935 Mus	092877 Mus mus	96966 SAG:apop	C011127 Mus mus	1 6

ALIGNMENTS

AUTHORS	BEEEBBACE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	BC011127	RESULT 1
L. (DASES I CO.1123) Strausberg,R.L., Feingold,B.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Mus musculus	Mus musculus (house mouse)	.MGC.	BC011127.1 GI:15029807	BC011127	IMAGE:4194107), complete cds.	Mus musculus ring finger protein 7, mRNA (cDNA clone MGC:19076	BC011127 1125 bp mRNA linear ROD 16-APR-2003		

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REMARK
COMMENT
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
MEDLINE
PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 24 Row: k Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (25-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: amg@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.hgsc.bcm.tmc.edu/cdna/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: BCM-HGSC
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Direct Submission
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/db_xref="LocusID:19823"
/translation="MADVEDGEEPCVLSSHSGSAGSKSGGDKMFSLKKWNAVAMWSWD
VECDTCAICRVQVMDACLRCQAENKQEDCVVVWGECNHSFHNCCMSLWVKQNNRCPLC
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                                                                                                                                                                                                                  codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                       gene="Rnf7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone="MGC:19076 IMAGE:4194107"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 month old male mouse.
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                                                                                                       Local
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WARNER LAMBERT CO
OS Unidentified
PN JP 2001526063-A/1
PD 18-DEC-2001
PF 15-DEC-1998 JP 2000525451
PF 19-DEC-1997 US 60/068179,11-SEP-1998 US 60/099840 PI
YI SUN
PC C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P17/02,A61P35/00,
PC A61P39/06,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC
PC G01N33/50,G01N33/68,C12N15/00,A61K37/02,C12N5/10,C12Q1/68,
PC G01N33/68,C12N15/00,A61K37/02,C12N5/00 CC
Strandedness Dubble;
CC Topology: Linear;
CC Jnote = 'Mouse SAG'
FT Key
FT CDS
FT mat Deptide 17. 355
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FT mat Deptide 17. 355
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                                                                                                                                                   /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Promotion of S-phase and cell growth under serum starvation by SAG/ROCZ/Rbx2/Hrt2, an E3 ubiquitin ligase component: association with inhibition of p27 accumulation

Mol. Carcinog: 30 (1), 37-46 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yeast homolog of human SAG/ROC2/Rbx2/Hrt2 is essential for cell growth, but not for germination: chip profiling implicates its role in cell cycle regulation oncogene 19 (24), 2855-2866 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Duan,H., Wang,Y., Aviram,M., Swaroop,M., Loo,J.A., Bian,J.,
Tian,Y., Mueller,T., Bisgaler,C.L. and Sun,Y.
SAG, a novel zinc RING finger protein that protects cells f
apoptosis induced by redox agents
Mol. Cell. Biol. 19 (4), 3145-3155 (1999)
                                                                                                                                                                Submitted (16-SEP-1998) Department
Parke-Davis, 2800 Plymouth Rd, Ann
Cocation/Qualifiers
1. .1140
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4 (bases 1 to 1140)
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the RING finger domain for apoptosis protection
Carcinogenesis 20 (10), 1899-1903 (1999)
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Mus musculus zinc RING finger protein
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Swaroop, M., Bian, J., Aviram, M., Duan, H., Bisgaier, C.L.,
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                                                                                                                                                                                                                                   Direct Submission
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/note="redox sensitive, metal binding; expression protects cells from apoptosis induced by redox compounds"
                                   /dev_stage="6-8 weeks"
17. .358
                                                                                                               /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6xCBA"
                                                                tissue_type="lung"
                                                                                   /sex="female"
                                                                                                db_xref="taxon:10090"
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                                                                                                                                                                                             of Molecular Biology,
Arbor, MI 48105, USA
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219370 bp DNA linear RC
Mus musculus chromosome 13 clone RP23-354J3, complete
AC123935
AC123935.4 GI:23462977
                                                                                                                                                                                                                                                                                       Submitted (02-OCT-2002) Genome Sequencing Center, 4444 Fo Parkway, St. Louis, MO 63108, USA On Oct 2, 2002 this sequence version replaced gi:22748547
                                                                                                                                                                                                                                                                                                                                                   Parkway, St. Louis, MO 63108, USA 4 (bases 1 to 219370) McPherson, J.D. and Waterston, R.H. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (05-JUN-2002) Genome Sequencing Parkway, St. Louis, MO 63108, USA 3 (Dases 1 to 219370)
MCPherson,J.D. and Waterston,R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 219370)
McPhorson,J.D. and Waterston,R.H.
The sequence of Mus musculus clone
Unpublished
                                                                                                                                     Center project name: M_BA0354J03
                                                                                                                                                                         Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                Center: Washington University Genome Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (13-SEP-2002) Genome Sequencing Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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McPherson, J.D. and Waterston, R.H.
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/product="zinc RING finger protein SAG"
/protein id="AAD25961.1"
/db_xref="GI:4588032"
/translation="MADVEDGEEPCVLSSHSGSAGSKSGGDKMFSLKKWNAVAMWSWD
VECDTCAICRYQVMDACLRCQAENKQEDCVVVWGECNHSFHNCCMSLWVKQNNRCPLC
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="13"
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source
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                                                                                                                                                                                                                                                                                                                                           where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84;
                                                                         numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-454N16 is from the RPCI-23 Mouse BAC Library constructed by the group of Pietter de Jong.

For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-APR-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Apr 16, 2003 this sequence version replaced gi:29825605.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: SC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 120515)
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1 45568 c 45395 g
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some 4, complete
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REFERENCE
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TITLE
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CE 2 (bases 1 to 244851)

RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boyuslavkiy, L., Boukgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Colarson, S., Barna, N., Camarata, J., Campopiano, A., Chang, J., Cook, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., PitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacChean, C., MacConald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKerran, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Myuyen, C., Nicol, R., Morbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Riley, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Traiamas, J., Tesfaye, S., Theodore, J., Viel, R., Voa, M., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Direct Submission

Direct Submission

M., Submitted (19, ADR-2002) Whitched Institute/MIT Center for Genome
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Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 244851)
Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
Bartien, V., Bloom, T.,
Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.
Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K.,
Collymore, A., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,
Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,
Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S.,
Graham, L., Grand-Pierre, N., Hafez, N., Hagpojan, D., Hagos, B.,
Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,
Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C.,
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Mus musculus (house mouse)
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 16, 2003 this sequence version replaced gi:28626759. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Mguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramassamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfave, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Niver, C., March, C., Tesfave, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Niver, C., March, C., Tolive, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Niver, C., March, C., Tesfave, G., Tesfave, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Niver, C., Tesfave, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: L24334
Center clone name: 91 A 16
Center clone name: 91 A 16
Center clone name: 91 A 16
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 243312 bases at least Q40
Consensus quality: 24327 bases at least Q30
Consensus quality: 24327 bases at least Q20
Insert size: 244251; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as soon as it is available and the accession number will be preserved.
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Quality coverage: 9.5 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: sequence_submissions@genome.wi.mit.edu
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Center: Whitehead Institute/ MIT Center for Genome
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                                    /note="assembly_fragment"
78957. .86294
                                                                                                            /note="assembly_fragment"
77810. .78856
                                                                                                                                                                                               vector_side:left"
                                                                                                                                                                                                                                              clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP24-91A16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Socation,
note="assembly_fragment"
                                                                                                                                                                                                                                                                       note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                      clone_lib="RPCI-24 Male Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
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76530: gap of 100 bp
77709: contig of 1179 bp in length
77809: gap of 100 bp
78856: contig of 1047 bp in length
78956: gap of 100 bp
86294: contig of 7338 bp in length
86394: gap of 100 bp
96039: contig of 9645 bp in length
96139: gap of 100 bp
228506: contig of 9645 bp in length
928506: contig of 13367 bp in length
228606: gap of 100 bp
1644551: contig of 16245 bp in length
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REFERENCE
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l (bases 1 to 612)
Wade, C.M., Kulbokas, E.J. III, Kirby, A.W., Zody, M.C., Mullikin, J.C.
Lander, E.S., Lindblad-Toh, K. and Daly, M.J.
The mosaic structure of variation in the laboratory mouse genome
Nature 420 (6915), 574-578 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BV071691 612 bp DNA SZ12P6546FB3.T0 CZECHII/Ei Mus musculus STS
                                                                                                                                                                                                                                 and the strain from which the particular read came. Thrate for these SNPs was estimated at approximately 98% Location/Qualifiers
                                                                                                                                                                                                                                                                      as STSs and 81,000~{
m SNPs} were annotated with alleles from C57{
m BL}/6{
m J} and the strain from which the particular read came. The validation
                                                                                                                                                                                                                                                                                                          annotated
                                                                                                                                                                                                                                                                                                                        WGS-discovery: Paired-end low-coverage whole genome shotgun reads were generated from 129S1/SvImu, C3H/HeJ, and BALB/CByJ. The WGS reads were placed uniquely on the MGSCv3 C57BL/6J assembly and SNP detection was carried out by SSAHA-SNP. 225,000 reads were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 6172521477
Fax: 6172580903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Research
320 Charles Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Kerstin Lindblad-Toh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BV071691.1 GI:31187486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer A: None
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: kersli@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Whitehead Institute
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54365 c 54122 g
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                                                                                                                                                          /organism="Mus musculus"
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/strain="CZECHII/Ei"
                                                                                                        /db xref="taxon:10090"
/map="- 10 22-541 63463278-63462744"
/clone_lib="CZECHII/Ei"
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                                                                    170 g
 Score 38;
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   DB 11;
. 7.6e-12;
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                Length 612;
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RESULT 8
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Submitted (20-DEC-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Dec 20, 2002 this sequence version replaced gi:17149550. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                   Direct Submission
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone
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Center clone name: 397_H_13
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Query Match
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TCTGGGGAGAGTGTAACCATTCCTTCCACAACTG 123
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37702
37802
389068
39068
39068
40236
401493
411493
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42692
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42971
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440711
46348
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33814
33914
35108
35208
36432
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43970: contig of 1100 bp
44070: gap of 100 bp
45150: contig of 1080 bp in
46447: gap of 100 bp
46447: gap of 100 bp
46447: gap of 100 bp
4881: contig of 1259 bp in
47608: contig of 1259 bp in
47608: gap of 100 bp
50240: contig of 1204 bp in
50140: gap of 100 bp
51544: contig of 1204 bp in
51644: gap of 100 bp
52828: gap of 100 bp
54157: contig of 1229 bp in
54257: gap of 100 bp
54750: contig of 1189 bp in
56731: contig of 1193 bp in
56731: contig of 1188 bp in
56831: gap of 100 bp
58119: gap of 100 bp
60525: contig of 1170 bp
60525: gap of 100 bp
604367: gap of 100 bp
61777; contig of 1174 bp in
61857: gap of 100 bp
61877: gap of 100 bp
61877: gap of 100 bp
61879: gap of 100 bp
                                                                                                                                                                                       65652: gap of 100 bp 166853: contig of 1201 bp 166953: gap of 100 bp 68145: contig of 1192 bp 168245: gap of 100 bp 69423: contig of 1178 bp 169523: gap of 100 bp 70737: contig of 1214 bp 170837: gap of 100 bp 70837: gap of 100 bp 10857: gap of 10857: gap 0657: ga
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35107: contig of 1194 bp i
35207: gap of 100 bp
36431: contig of 1224 bp i
36331: gap of 100 bp
37701: contig of 1170 bp i
37701: gap of 100 bp
37701: gap of 100 bp
38967: gap of 100 bp
40235: contig of 1168 bp i
40335: gap of 100 bp
40335: gap of 100 bp
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                                                                                                                                                gap of
                                                                Score 34;
Pred. No.
                                           Mismatches
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g of 1160 bp in length
f 100 bp
g of 1157 bp in length
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provided by the submittor.
This sequence will be replaced
by the finished sequence as soon as it is available and

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REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RRS Birren, B., Linton, L., Musbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Bnukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cook, A., Cooke, P., Fizhugh, W., Gage, D., Galegan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Oliver, J., Peterson, K., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Sernas, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Viel, R., Voa, M., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. E., W.J., Young, G., Shirback, M., Kiley, R., Key, J., Young, G., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (14-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                              Contact: sequence submissions@genome.wi.mit.edu

Center project Information

Center roject name: 119568

Center clone name: 200 C 17

Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 184259 bases at least Q30

Consensus quality: 18510 bases at least Q30

Consensus quality: 18510 bases at least Q30
consists of 10 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 187353)
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                                                                                                                                                                                                                Insert size: 194000; agarose-fp
Insert size: 186453; sum-of-contigs
Quality coverage: 7.4 in Q20 bases; agarose-fp
Quality coverage: 7.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
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BD077705
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5'EST of secreted protein
                                                    BD077705.1 GI:22623308
JP 2001512016-A/291.
                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                     Homo sapiens (human)
                                                                                                                                                                                      TGCCATCTGCAGGGTCCAGGTGATGGATGCCTG 46073
                                                                                                                                                                                                   TGCCATCTGCAGGGTCCAGGTGATGGATGCCTG 45
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vector_side:right"
34855 c 36129 g
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP23-200C17"
                                                                                                                                                                                                                                                                                                                                            note="assembly_fragment
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629: contig of 629 bp in length
729: gap of 100 bp
750: contig of 21 bp in length
850: gap of 100 bp
3212: contig of 2182 bp in length
3312: gap of 100 bp
6908: contig of 3596 bp in length
7008: gap of 100 bp
14344: contig of 7426 bp in length
14534: gap of 100 bp
32181: contig of 17647 bp in length
14534: gap of 100 bp
32181: contig of 100 bp
32181: contig of 100 bp
32181: contig of 100 bp
32181: gap of 100 bp
32181: gap of 100 bp
31167: contig of 18866 bp in length
51267: gap of 100 bp
72970: gap of 100 bp
72970: gap of 100 bp
149992: contig of 77022 bp in length
150092: gap of 100 bp
187353: contig of 37261 bp in length.
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                                                                                                                                                                                                                                                                                                        905 others
                                                                                                                                                                                                                                         Indels
                                                                                                                   linear
                                                                                                        and
                                                                                                       PAT 27-AUG-2002 other mesodermal
                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                       Gaps
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             LOCUS
DEFINITION
                                      RESULT 11
AX282592
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AUTHORS
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                                                                                                                                                                                                  ORIGIN
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                                                                                                                                                                                                                                                                              FEATURES
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ACCESSION
                                                                                                                                            Query Match
Best Local Similarity
Matches 32; Conserv
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                                                                                                                                                                                                                                                                   source
                                                                                           174 GCCATCTGCAGGGTCCAGGTGATGGATGCCTG
                                                                                                           14 GCCATCTGCAGGGTCCAGGTGATGGATGCCTG 45
AX282592
Sequence
AX282592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent: JP 2001512016-A 291 21-AUG-2001; GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 224)
Edwards, J.B.D.M., Duclert, A. and Lacroix, B.
5'EST of secreted protein expressed in muscles and other mesodermal
                                                                                                                                                                                                                                                                                             tissues
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fisc_feature
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id W81645
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17 2001512016-A/291
21-AUG-2001
31-JUL-1998 JP 2000505295
01-AUG-1997 US 08/905134
01-AUG-1997 US 08/905134
OTEAN BAPTISTE DUMAS MILNE EDWARDS, AYMERIC DUCLERT, BRUNO
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id W06951
                                                                                                                                              Conservative
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misc_feature
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               7
                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
60 c 83 g 3
                                                                                                                                                                                                                                                                              ocation/Qualifiers
            342 bp
from Patent WO0175145.
                                                                                                                                                           25.2%;
100.0%;
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                                                                                                                                                           Score 32; DB 6; 1
Pred. No. 4.1e-08
                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                               Mismatches
                                                                                                                                                                                                              38
                          DNA
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                                                                                                                                               0,
                                                                                                                                                                        Length 224
                                                                                                                                               Indels
                           linear
                                                                                                                                                                                                                others
                           PAT 02-NOV-2001
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FEATURES

source

RESULT 10 BD077705

Gaps

0

SOURCE KEYWORDS VERSION ACCESSION DEFINITION

ORGANISM

В Ş

46105 13 Matches

BASE COUNT ORIGIN

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REFERENCE
AUTHORS
TITLE
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ORGANISM
   BASE COUNT
ORIGIN
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ACCESSION
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TITLE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 GCCATCTGCAGGGTCCAGGTGATGGATGCCTG 45
                                                                                                                                                                                                                                                                                                   Submitted (10-APR-1999) Lineberger Comprehensive Cancer Center, University of North Carolina at Chapel Hill, Mason Farm Rd. and Manning Dr., Chapel Hill, NC 27599-7295, USA
                                                                                                                                                                                                                                                                                                                                                                 Ohta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ubiquitin ligase assay Patent: WO 0175145-A 7 11-OCT-2001; Rigel Pharmaceuticals, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                            MO1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelebstomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 342)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens RING finger
AF142060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF142060.1 GI:4809217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF142060
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AX282592.1
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                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 342)
a,T., Michel,J.
                                                                                                                                                                                                                                                                                                                                                                                                                        T., Michel,J.J., Schottelius,A.J. and Xiong,Y., a homolog of APC11, represents a family of cu an associated ubiquitin ligase activity cell 3 (4), 535-541 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens
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                                                                                                                                                                                                                                                                                                                                                            Michel, J. and Xiong, Y.
                             QQDWVVQRIGK"
                                          /translation="MADVEDGEETCALASHSGSSGSTSGGDKMFSLKKWNAVAMWSWD
VECDTCAICRVQVMDACLRCQAENKQEDCVVVWGECNHSFHNCCMSLMVKQNNRCPLC
                                                                     /codon_start=1
/product="RING finger protein"
/protein_id="AAD30147.1"
/db_xref="GI:4809218"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
84 c 108 g 6
                                                                                                                                   /note="Cullin partnering protein with
ligase activity"
                                                                                                                                                                 gene="ROC2"
                                                                                                                                                                                                                                         organism="Homo sapiens"
|mol_type="mRNA"
                                                                                                                                                                                                                                                                                    Socation/Qualifiers
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                                                                                                                                                                                             gene="ROC2"
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Pred. No.
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               68 t
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4e-08;
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BT007348
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                                                                                        Query Match
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
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                                                    32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the Sall and HindIII sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after Sall site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Clone distribution: http://bioinfo.clontech.com/orfclones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (13-MAY-2003) BD Biosciences Clontech, Circle, Palo Alto, CA 94303, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 342)
Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Koundinya, M., Raphael, J., Moreira, D., Kelley, T., LaBaer, J., Lin, Y., Phelan, M., and Farmer, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vector
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Koundinya, M., Raphael, J., Moreira, D., Kelley, T., Phelan, M. and Farmer, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 342)
Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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FLI_CDNA.
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GCCATCTGCAGGGTCCAGGTGATGGATGCCTG 45
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                                                    Conservative
                                                                                                                                                  82
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                                                                                                                                                                                    /product="ring finger protein 7"
/protein id="AAP36012.1"
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VECDTCAICRVQVMDACLRCQAENKQEDCVVVWGECNHSFHNCCMSLWVKQNNRCPLC
                                                                                                                                                  QQDWVVQRIGK"
83 c
                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GH00912X1.0"
                                                                                                                                                                                                                                                                                                                                                                   collection"
                                                                                                                                                                                                                                                                                                                           note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                   clone_lib="BD Creator(TM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
                                                                                                                                                                                                                                                                                         codon start=1
                                                                                                                                                                                                                                                                                                                           lab_host="DH5alpha T1 resistant"
10te="Vector: pDNR-Dual"
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                                                                    25.2%;
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                                                  Score 32; DB
Pred. No. 4e-
0; Mismatches
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                                                                        DB 9;
. 4e-08;
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4e-08;
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RESULT 15
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                               PR PR PR OS
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SAG:apoptosis sensitivity
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                                                                                                                                                                                                                                                                                                                                                                unidentified
                                                                                                                                                                                                                                                                                                                                                                                        unidentified
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BD096981.1 GI:22642569
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JP 2001526063-A/2.
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SUN
C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P17/02,A61P35/00,
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                                                                                                                            Unidentified
JP 2001526063-A/16
18-DEC-2001
                                                                    15-DEC-1998 JP 2000525451
19-DEC-1997 US 60/068179,11-SEP-1998 US
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Pred. No. 4e-08;
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Best Local S
Matches 32
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Best Local S
Matches 32
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BD096985.1 GI:22642573
JP 2001526063-A/20.
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PC A61P43/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21
,C12NS/10,C12Q1/68,
PC G01N33/50,G01N33/68,C12N15/00,A61K37/02,C12N5/00 CC
Strandedness: Double;
CC Topology: Linear;
CC SAG:apoptosis sensitivity gene
PH Key Location/Qualifiers
FT CDS
1.339
FT CDS
1.339.
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PC A61P43/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC
,C12N5/10,C12Q1/68,
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GCCATCTGCAGGGTCCAGGTGATGGATGCCTG 45
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18-DEC-2001
15-DEC-1998 JP 2000525451
19-DEC-1997 US 60/068179,11-SEP-1998 US
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larity 100.0%;
Conservative
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                                                                                                  /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
a 155 c 201 g 192
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ORGANISM
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VERSION
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BD096987
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PN JP 2001526063-A/21
PD 18-DEC-2001
PF 15-DEC-1998 JP 200525451
PF 15-DEC-1998 US 60/068179,11-SEP-1998 US 60/099840
PR 19-DEC-1997 US 60/068179,11-SEP-1998 US 60/099840
PC C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P17/02,A61P
PC A61P39/06,
PC A61P39/06,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/2
PC A61P43/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/2
PC G01N33/50,G01N33/68,C12N15/00,A61K37/02,C12N5/00 CC
Strandedness: Double;
PC Topology: Linear;
CC Topology: Linear;
CC SAG:apoptosis sensitivity gene
PH Key
CC SAG:apoptosis sensitivity gene
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CD SAG:apoptosis sensitivity gene
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CD SAG:apoptosis sensitivity gene
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CD SAG:apoptosis sensitivity gene
SAG:apoptosis sensitivity gene
Patennt: JP 2001526063-A 22 18-DEC-2001;
WARNER LAMBERT CO
OS Unidentified
PN JP 2001526063-A/22
PD 18-DEC-2001
PF 15-DEC-1998 JP 2000525451
PR 19-DEC-1997 US 60/068179,11-SEP-1:
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JP 2001526063-A/21.
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SAG:apoptosis sensitivity gene
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              18-DEC-2001
15-DEC-1998 JP 2000525451
19-DEC-1997 US 60/068179,11-SEP-1998
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A61P43/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
154 c 201 g 19
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Pred. No. 4e-08;
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OS Unidentified
PN JP 2001526063-A/23
PD 18-DEC-2001
PF 15-DEC-1998 JP 2000525451
PF 15-DEC-1997 US 60/068179,11-SE
YI SUN
PC C12N15/09,A61K31/711,A61K38/00,A6
PC A61P43/00,C07K14/47,C07K16/18,C12
PC A61P43/00,C07K14/47,C07K16/18,C12
PC G01N33/50,G01N33/68,C12N15/00,A61
Strandedness: Double;
PC Topology: Linear;
PC SAG:apoptosis sensitivity gene
PC SAG:apoptosis sensitivity gene
PT CDS
PT CD
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PC A61P39/06,
PC A61P39/06,
PC A61P33/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC
PC G01N33/50,G01N33/68,C12N15/00,A61K37/02,C12N5/00 CC
Strandedness: Double;
CC Topology: Linear;
CC SAG:apoptosis sensitivity gene
FH Key Location/Qualifiers
FT CDS 1.339
FT mat_peptide 1.339.
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ilarity 100.0%;
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15-DEC-1998 JP 2000525451
19-DEC-1997 US 60/068179,11-SEP-1998 US
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peptide 1. .339.
Location/Qualifiers
                                                                                                                                                              /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon;32644"
155 c 201 g 19
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Pred. No. 4e-
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Gaps
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KEYWORDS
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PN JP 200152603-A/24
PD 18-DEC-2001
PF 15-DEC-1998 JP 2000525451
PF 15-DEC-1998 JP 2000525451
PF 15-DEC-1997 US 60/068179,11-SEP-1998 US 60/099
YI SUN
PC C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P17/02,A
PC A61P39/06,
PC A61P43/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N
PC A61P43/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N
PC G01N33/50,G01N33/68,C12N15/00,A61K37/02,C12N5/00 CC
Strandedness: Double;
PC G01N33/50,G01N33/68,C12N15/00,A61K37/02,C12N5/00 CC
Strandedness: Double;
CC Topology: Linear;
CC SAG:apoptosis sensitivity gene
FH Key
Location/Qualifiers
FT CDS
1. .339
FT mat_peptide 1. .339.
   SAG: apoptosis sensitivity gene
Patent: JP 2001526063-A 25 18-DEC-2001;
WARNER LAMBERT CO
OS Unidentified
PN JP 2001526663-A/25
PD 18-DEC-2001
PF 15-DEC-1998 JP 2000525451
PR 19-DEC-1997 US 60/068179,11-SEP-1
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                                                                                                                                                              unidentified unidentified unclassified.
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JP 2001526063-A/25.
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WARNER LAMBERT CO
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JP 2001526063-A/24.
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Unidentified
JP 2001526063-A/25
18-DEC-2001
15-DEC-1998 JP 2000525451
19-DEC-1997 US 60/068179,11-SEP-1998 US
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A61P43/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
155 c 201 g 19
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ACCESSION
VERSION
KEYWORDS
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BD096991
LOCUS
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Query Match
Best Local (
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TITLE
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WARNER LAMBERT CO
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PD 18-DEC-2001
PF 15-DEC-1998 UP 2000525451
PR 19-DEC-1997 US 60/068179,11-SEP-1998 US 60/099840 PI
PR 19-DEC-1998 US 60/068179,11-SEP-1998 US 60/099840 PI
PR 19-DEC-1997 US 60/068179,11-SEP-1998 US 60/09880 PI
PR 19-DEC-1997 US 60/068179,11-SEP-1998 US 60/09880 PI
PR 19-DEC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strandedness: Double;
CC Topology: Linear;
CC SAG:apoptosis sens:
FH Key
FT CDS
1.
FT mat_peptide 1.
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JP 2001526063-A/26.
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32; Conserv
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PC A61P39/06,
PC A61P34/06,
PC A61P34/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC
C12N5/10,C12Q1/68,
PC G01N33/50,G01N33/68,C12N15/00,A61K37/02,C12N5/00 CC
Strandedness: Double;
CC Topology: Linear;
CC Topology: Linear;
CC SAG:apoptosis sensitivity gene
FH Key
FT CDS
SAG:apoptosis sensitivity gene
FH Key
FT CDS
1.339
FT mat_peptide 1.339.
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Location/Qualifiers
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A61P39/06,
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25.2%;
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Score 32; DB 6;
Pred. No. 4e-08;
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Pred. No.
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4e-08;
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Conservative

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Mismatches

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Gaps

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14

GCCATCTGCAGGGTCCAGGTGATGGATGCCTG

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REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                LOCUS
DEFINITION
ACCESSION
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ACCESSION
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KEYWORDS
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BD096992
LOCUS
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BD096994
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TITLE
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Patent: JP 2001526063-A 29 1
WARNER T.CO
OS Unidentified
PN JP 2001526063-A/29
PD 18-DEC-2001
PF 15-DEC-1998 JP 20005254
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SAG:apoptosis sensitivity
                                                                    Sun
                                                                                                                  BD096994.1 GI:22642582 JP 2001526063-A/29.
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SAG:apoptosis sensitivity gene.
                                                                                                          unidentified
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                                                                                        unclassified
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                                                                             (bases 1 to 754)
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15-DEC-1998 JP 2000525451
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100.0%; Pr
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Pred. No. 4e-08;
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DEFINITION
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BD096995
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TITLE
JOURNAL
Query Match

Best Local Similarity

Matches 32; Conserv
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YI SUN
PC (S12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P17/02,A61P35/00,
PC A61P39/06,
PC A61P39/06,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC,C12N5/10,C12Q1/68,
PC G01N33/50,G01N33/68,C12N15/00,A61K37/02,C12N5/00 CC
Strandedness: Double;
CC Topology: Linear;
CC SAG: apoptosis sensitivity gene
FH Key
PT CDS
1 339
FT mat_peptide 1 339.
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WARNER LAMBERT CO
OS Unidentified
PN JP 2001526063-A/30
PD 18-DEC-2001
PF 15-DEC-1998 JP 20005;
PR 19-DEC-1997 US 60
YI SUN
PC C12N15/09, A61K31/711
PC A61P43/00, C07K14/47,
PC A61P43/00, C07K14/47,
PC A61P43/00, G01N33/68,
PC G01N3/50, G01N33/68,
PC G01N3/50, G01N33/68,
PC G01N3/50, G01N3/68,
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2001526063-A/30.
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                                                                                                                                    206
                                                                                                                                                                                                                                                                                                      dedness. Finear;
Topology: Linear;
SAG:apoptosis sensitivity gene
Location/Qualifiers
  25.2%; Scilarity 100.0%; P
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A61P43/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC
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18-DEC-2001
15-DEC-1998 JP 2000525451
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
155 c 201 g 192
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0; Mismatches
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                                                                                                                                                                                                                                                                             Submitted
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                                                                                                                                                                                                                                         Sun,
                                                                                                                                                                                                                                                                                                                                                                            Duan, H., Tsvetkov, L.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Yeast homolog of human SAG/ROC2/Rbx2/Hrt2 is essential for cell growth, but not for germination: chip profiling implicates its role in cell cycle regulation
Oncogene 19 (24), 2855-2866 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Expression, purification, and biochemical characterization of SAG, a RING finger redox-sensitive protein Free Radical Biol. Med. 27, 193-202 (1999)

4 (bases 1 to 754)
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Swaroop, M., Bian, J., Aviram, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alterations of SAG mRNA in human cancer cell lines: requirement the RING finger domain for apoptosis protection Carcinogenesis 20 (10), 1899-1903 (1999)
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Tian, Y., Mueller, T., Bisgaier, C.L. and Sun,
SAG, a novel zinc RING finger protein that
apoptosis induced by redox agents
Mol. Cell. Biol. 19 (4), 3145-3155 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Swaroop, M., Wang, Y., Miller, P., Duan, H., Jatkoe, T., Madore, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/note="redox sensitive, metal binding; expression protects
cells from apoptosis induced by redox compounds"
                                                                                                                                                                      (16-SEP-1998) Department is, 2800 Plymouth Rd, Ann Location/Qualifiers
                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="3"
                               function="growth promotion"
                                                            _line="HeLa, D98/AH-2, HPRT-"
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ein SAG mRNA,
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cbor, MI 481
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                                                                                                                                                                                                                                                                                                                                                                                                                           cione distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 12 Row: h Column: 14
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S.,
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck,
Muzny,D.M., Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium of the Consortium of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (25-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 816)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg, R.
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/product="rinc RING finger protein SAG"
/protein id="AAD25962.1"
/db_xref="GI:4588034"
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VECDTCAICEXCUMDACLRCQAENKQEDCVVVWGECNHSFHNCCMSLWVKQNNRCPLC
                                                                                                       tissue type="Brain, anaplastic oligodendroglioma with 1p/19q loss"
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155 c
                                                                                                                                                                                 mol_type="mRNA"
/db_xref="Locus10:9616"
/db_xref="Laxon:9606"
/clone="MGC:17274_IMAGE:4177613"
note="Vector: pCMV-SPORT6"
                                          'lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
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                                                                     lib="NCI_CGAP_Brn67"
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Pred. No.
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 GCCATCTGCAGGGTCCAGGTGATGGATGCCTG 45
                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 21 Row: o Column: 13 This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BC005966
BC005966.1 GI:13543635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene Collection (MGC), Cance Institute, 31 Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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/db_xref="GI:14250389"
/tahslation="MADVEDGEETCALASHSGSSGSKSGGDKMFSLKKWNAVAMWSWD
/trahslation="MADVEDGEETCALASHSGSSGSKSGGDKMFSLKKWNAVAMWSWD
VECDTCAICRVQVMDACLRCQAENKQEDCVVVWGBCNHSFHNCCMSLMVKQNNRCPLC
               /codon start=1
/product="ring finger protein
/protein id="AAH05966.1"
/db_xref="GI:13543636"
                                                                                                                                                   /tissue_type="Kidney, hypernephroma"
/clone_Tib="NIH_MGC_58"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                             Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www-shgc.stanford.edu
(Dickson, Mark) mcd@paxil.stanford.edu
M., Schmutz, J., Grimwood, J., Rodriquez, A.,
translation="MADVEDGEETCALASHSGSSGSKSGGDKMFSLKKWNAVAMWSWD/
                                                                                                                                                                                                            db_xref="taxon:9606"
/clone="MGC:14618 IMAGE:4069078"
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                                                                                                                            note="Vector: pDNR-LIB"
                                                                                                                                                                                                                                                         db_xref="LocusID:9616"
                                                                                                                                                                                                                                                                                mol_type="mRNA"
                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
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Pred. No. 4e-08;
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3 IMAGE:4069078,
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AC118192
AC118192.1 GI:20147957
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP
                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (01-JUL-1999) Department of Biochemistry, Kyungpook
National University, Taegu 702-701, Korea
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Bae, Y.-S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein kinase CKII interacts with and phosphorylates the SAG protein containing ring-H2 finger motif Biochem. Biophys. Res. Commun. 263 (3), 743-748 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                              pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Son, M.-Y., Park, J.-W., Kim, Y.-S.,
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                                                                                                                                                                           GCCATCTGCAGGGTCCAGGTGATGGATGCCTG 45
                                                                                                                                                         GCCATCTGCAGGTCCAGGTGATGGATGCCTG
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                                                                                                                                                                                                                                                                                                  228
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175 c
                                                                                                                                                                                                                                                                                              QQDWVVQRIGK"
185 c
                                                                                                                                                                                                                                                                                                                /codon_start=1
/product="ring finger protein CKBBP1"
/product="ring finger protein CKBBP1"
/protein id="AAD55984.1"
/db_xref="GI:5917674"
/translation="MADVEDGEETCALASHSGSSGSKSGGDKMFSLKKWNAVAMWSWD
/translation="MADVEDGEETCALASHSGSSGSKSGGDKMFSLKKWNAVAMWSWD
VECDTCAICEVQVMDACLRCQAENKQEDCVVVWGECNHSFHNCCMSLWVKQNNRCPLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VECDTCAICR VQVMDACLRCQAENKQEDCVVVWGECNHSFHNCCMSLWVKQNNRCPLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                         note="SAG; contains an H2 ring finger motif"
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100.0%; Pr
                                                             187353 bp
clone RP23-200C17,
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                                                               DNA linear HTG
WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                    DB 9;
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4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kang, S.-W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 187353)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-200C17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (14-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://ftp.genome.washington.edu/RM/RepeatMasker.html
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by the finished sequence as soon as it is available and the accession number will be preserved.

1 629: contig of 629 bp in length
630 729: gap of 100 bp '
730 750: contig of 21 bp in length
751 850: gap of 100 bp
851 3212: contig of 2362 bp in length
3213 3312: gap of 100 bp
3313 6908: contig of 3596 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                         is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 184259 bases at least Q40 Consensus quality: 1851710 bases at least Q30 Consensus quality: 186169 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: L19568
Center clone name: 200 C_17
Center Summary Statistics
Sequencing vector: Plasmid; n.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality coverage: 7.4 in Q20 bases; Quality coverage: 7.7 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insert size: 194000; agarose-fp
Insert size: 186453; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-seq.wi.mit.edu
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sum-of-contigs
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AC095698/c
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Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalabechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
                                                                                                                                                                                                                                                                                      AC095698 254832 bp DNA linear HTG 09-
Rattus norvegicus clone CH230-9D13, WORKING DRAFT SEQUENCE
                                                                                                                                                                                                  Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                  HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                              Rattus.
                                                                                                                                                             Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammālia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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vector_side:1
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/db_xref="taxon:10090"
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7: contig of 18886 bp in length
7: gap of 100 bp
0: contig of 21603 bp in length
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contig of 37261 bp
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contig of 7426 bp in length
gap of 100 bp
contig of 17647 bp in length
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Pred. No. 3.6e-(
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of 77022 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockeell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Diyya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Dubbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Ferseer, C.M., Gabisi, A., Gante, R., Garcia, A., Garrer, T., Garza, M., Gubrara, W., Gunaratne, P., Haaland, M., Hamilton, C., Hamilton,
                                                                                                                                                                   of Molecular and Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 9, 2002 this sequence version replaced gi:23267899.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 254832)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Worley, K.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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                                  Center: Baylor College of Medicine Center code: BCM
                                                                                                              ----- Genome Center
   site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                 VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 32
BD096984
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ACCESSION
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                                                                    AUTHORS
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JOURNAL REFERENCE

TITLE

AUTHORS TITLE JOURNAL

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               146354 CCATCTGCAGGTCCAGGTGATGCATGCCTG 146324
Sun, Y.
SAG:apoptosis sensitivity gene
Patent: JP 2001526063-A 19 18-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 CCATCTGCAGGGTCCAGGTGATGGATGCCTG
                                                                                                                                                                                                                                    754 bp SAG:apoptosis sensitivity gene.
                                                                                                                                                 unidentified
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JP 2001526063-A/19.
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
                                                                                                                      unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63080
                                                                                               (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: GDBC
Center clone name: CH230-9D13
Center clone name: CH230-9D13
Center clone name: CH230-9D13
Consensus quality: 238918 bases at least Q30
Consensus quality: 241069 bases at least Q30
Consensus quality: 24304 bases at least Q20
Estimated insert size: 243228; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
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complement(253801.
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clone_end:T7
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233357. .235284
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clone_end:Sp6
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253718. .254832
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/db_xref="taxon:10116"
/clone="CH230-9D13"
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58350 c 57410 g 64047 t 11945 others
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100.0%; Pred. No. 1.5e-07;
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BASE COUNT
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TITLE
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Best Local 9
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                                                                                                                                                 AL Patent: JP 2001526063-A 28 18-DEC-2001;

WARNER LAMBERT CO
OS Unidentified
PN JP 2001526063-A/28
PD 18-DEC-2001
PF 15-DEC-1998 JP 2000525451
PR 19-DEC-1997 US 60/068179,11-SEP-1998 US 60/099840 PI
YI SUN
PC C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P17/02,A61P35/00,
PC A61P39/06,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC
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PC A61P33/00,C01N33/68,C12N15/00,A61K37/02,C12N5/00 CC
Strandedness Double;
CC Topology: Linear;
CC Topology: Linear;
CC SAG.apoptosis sensitivity gene
FH Key: apoptosis sensitivity gene
FH Key: apoptosis sensitivity gene
FH Key: mat_peptide 1.339
FT mat_peptide 1.339.
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OS Unidentified
PN JP 2001526063-A/1
PD 18-DEC-2001
PF 15-DEC-1998 JP 20
PR 19-DEC-1997 US
YI SUN
PC C12N15/09,A61K31/-
PC A61P33/06,
PC A61P33/06,
PC A61P33/06,
PC G01N33/50,G01N33/,
C12N5/10,C12Q1/68,
PC G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N33/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/50,G01N3/
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SAG:apoptosis sensitivity gene.
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     207
                                                                                                                                                                                                                                                                                                                                                                                                           C12N15/09, A61K31/711, A61K38/00, A61K48/00, A61P17/02, A61P35/00
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18-DEC-2001
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19-DEC-1997 US 60/068179,11-SEP-1998 US
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ocation/Qualifiers
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Taenzer, S. and Platzer, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (25-APR-2002) Genome Analysis, Institute or Notice Submitted (25-APR-2002) Genome Analysis, Institute or Notice Submitted (25-APR-2002) Genome Analysis, Institute or Notice Submission (25-APR-2002) Genome Analysis (25-APR-2002
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Taenzer, S. and Platzer, M.
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NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                           Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality levels above 40 are expected 1 error in 10,000 bp.
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Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of re
Assembly program: Phrap; version 0.990329
Consensus quality: 140730 bases at least Q40
Consensus quality: 143576 bases at least Q30
Consensus quality: 145595 bases at least Q20
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Muzny, D. Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Barastead, M., Bendaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Carder, K., Cavazos, I., Ceasar, H., Center, A., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Coyte, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Daval, B., Baves, K., Egan, A., Esoutto, M., Bugene, C., Evans, C.A., Falls, T., Fan, G., Egan, A., Esoutto, M., Bugene, C., Evans, C.A., Falls, T., Fan, G., Francer, S., Gabisi, A., Ganta, R., Garcia, M., Gebregeorgia, E., Geer, K., Gill, R., Grady, M., Guerra, W., Handerson, N., Hernandez, J., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Harvey, Y., Harlandez, J., Harderson, M., Hennandez, J., Harderson, M., Hennandez, J., Harlandez, 
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AC125667.5 GI:30522767
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC125667 250425 bp DI Rattus norvegicus clone CH230-21C17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
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119806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="RP32-4G14"
/clone_lib="RPCI-32 BAC Library"
| 31830 c 31870 g 41911 t 9
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/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Rattus norvegicus"
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25464: gap of unknown length
38093: contig of 12629 bp in length
38193: gap of unknown length
83977: contig of 45604 bp in length
83897: gap of unknown length
90673: contig of 6776 bp in length
90773: gap of unknown length
107588: contig of 16815 bp in length
107688: gap of unknown length
112170: contig of 4482 bp in length
112270: gap of unknown length
112270: gap of unknown length
113905: gap of unknown length
119905: gap of unknown length
119905: gap of unknown length
139049: contig of 7535 bp in length
139049: contig of 18044 bp in length
146503: contig of 8454 bp in length
146603: gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30;
Pred. No.
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REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

TITLE JOURNAL REFERENCE

AUTHORS TITLE

JOURNAL

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Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jackson, L., Jalang, H., Johnson, B., Johnson, R., Johnson, R., Karpathy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Loulseged, H., Lozado, R. J., Lu, X., Ma, Mangum, A., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Mankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pul, -L., Pluzo, M., Outroy, J., Ren, Y., Reuter, M., Reighr, R., Reigh, R., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Reeves, K., Regiar, M.A., Reigh, R., Rives, G., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Shethy, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Steinie, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Tabor, P., Taylor, C., Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Wang, O., Wang, S., Willson, R., Wiess, R., Wooden, H., Worley, K., Willson, R., Wiess, R., Walk, S., Ven, J., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, J., Zhou, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Meinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, X77030, USA
On May 10, 2003 this sequence version replaced gi:24819649.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (29-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 250425)
Rat Genome Sequencing Consortium.
                                                may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 250425).
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Center project name: GGKL
Center clone name: CH230-21C17
Center clone name: CH230-21C17
Center clone name: CH230-21C17
Center clone name: Atlas 3.0;
Assembly program: Atlas 3.0;
Consensus quality: 241733 bases at least Q40
Consensus quality: 244050 bases at least Q30
Consensus quality: 245337 bases at least Q20
Estimated insert size: 249556; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimat Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu Center: Baylor Co Center code: BCM Web site: http:// _____ Project Information ----- Genome Center College of Medicine Q20 bases; sum-of-contigs estimation

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KEYWORDS
SOURCE
ORGANISM
                                                            REFERENCE
                                                                                                                                                                                                                  REFERENCE
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ORIGIN
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                                                                                JOURNAL
MEDLINE
PUBMED
                       AUTHORS
TITLE
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Best Local
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Swaroop,M., Gosink,M. and Sun,Y. SAG/ROC2/Rbx2/Hrt2, a component structure, a splicing variant, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30;
                                                                                                              Duan, H., Wang, Y., Aviram, M., Swaroop, M., Loo, J.A., Bian, J., Tian, Y., Mueller, T., Bisgaier, C.L. and Sun, Y. SAG, a novel zinc RING finger protein that protects cells f. apoptosis induced by redox agents

MIN. Cell. Biol. 19 (4), 3145-3155 (1999)
                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                  Homo sapiens SAG splice
AF312226
                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                         Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                              AF312226.1 GI:13649605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "working draft" sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATGTCAAGCTGAAAACAAGCAAGAAGACT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70050 a
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                                                                                                                                                                                                              (bases 1 to 674)
                                                         (bases 1 to 674)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.6%; Score 30; DB 2; L
llarity 100.0%; Pred. No. 6.2e-07;
Conservative 0; Mismatches 0;
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247927. .:
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clone_end:Sp6"
2873. ..3401
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clone_end:T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="wgs_end_extension
clone end:T7"
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clone_end:T7"
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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                                                        Strandedness: Double;
CC Topology: Linear;
CC SAG:apoptosis sens
FH Key
FT CDS
FT CDS
FT mat_peptide 1:
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29; Conser
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PC G01N33/50,G01
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Patent: JP 2001526063-A 8 18-DEC-2001;
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                                                                                                                                                                                                                                                                                                                                                                              unclassified.
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15-DEC-1998 JP :
19-DEC-1997 US
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                                                                                                    SAG:apoptosis sensitivity
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CLDDHR"
/organism="unidentified"
/mol_type="genomic DNA"
                                            ocation/Qualifiers
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/product="SAG Splice_variant"
/protein_id="AAK37450.1"
/db_xref="GI:1364966"
/translation="MADVEDGEETCALASH8GSSGSKSGGDKMFSLKKWNAVANWSWD
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/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="3"
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WARNER LAMBERT CO
OS Unidentified
PN JP 200152603-A/17

PD 18-DEC-1998 JP 200525451
PF 15-DEC-1998 UP 60/068179,11-SEP-1998 US 60/099840
PR 19-DEC-1997 US 60/068179,11-SEP-1998 US 60/099840
PR 19-DEC-
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                                                                                          78AG:apoptosis sensitivity
BD096983
BD096983 GI:22642571
JP 2001526063-A/18.
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SAG:apoptosis sensitivity
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Patent: JP 2001526063-A 17 18-DEC-2001;
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(bases 1 to 754)
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
_155 c 201 g 19
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Pred. No. 2.9e-06;
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CE 2 (bases 1 to 112321)

RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., RS Birren, B., Linton, L., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Galagan, J., Gardyna, S., Ferreira, P., FitzHugh, W., Galagan, L., Gardyna, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kambat, A., Kells, C., LaRocque, K., Jones, C., Karatas, A., Kells, C., LaRocque, K., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Riaback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Straugs, N., Schyannaia, A., Talamas, J., Teofavo, C., Thodox, T., Johnson, R., Schupback, R., Straugs, N., Schyannaia, A., Talamas, J., Teofavo, C., Thodox, R., Schupback, R., Straugs, N., Schyannaia, A., Talamas, J., Teofavo, C., Thodox, R., Schupback, R., Straugs, N., Schyannaia, A., Talamas, J., Teofavo, C., Thodox, R., Schupback, R., Schupback, R., Stange, Thodox, R., Schupback, R., Stange, Thodox, R., Stojanovic, N., Schupback, R., Stange, Thodox, R., Schupback, R., Stange, Thodox, R., Stange, T
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OS Unidentified
PN JP 200152663-A/18
PD 18-DEC-2001
PF 15-DEC-1998 JP 2000525451
PF 15-DEC-1998 US 60/068179,11-SEP-1998 US 60/099
YI SUN
PC C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P17/02,A
PC A61P39/06,
PC A61P43/00,CO7K14/47,CO7K16/18,C12N1/15,C12N1/19,C12N
PC G12N3/50,G01N33/68,C12N15/00,A61K37/02,C12N5/00 CC
Strandedness: Double;
PC Topology: Linear;
CC Topology: Linear;
CC SAG:apoptosis sensitivity gene
FH Key
FT CDS
PT CDS
1. 339
PT mat_peptide 1. 339
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Mus musculus clone RP23-397H13,
AC103666
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Birren,B., Nusbaum,C. and Lande,
Mus musculus, clone RP23-397H13
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SAG:apoptosis sensitivity gene
Patent: JP 2001526063-A 18 18-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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Mammalia; Eutheria; Rodentia;
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/mol_type="genomic DNA"
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•	TITLE JOURNAL COMMENT	TITLE JOURNAL REFERENCE AUTHORS					
http://ftp.genome.washington.edu/RM/RepeatMasker.html	Cook, A., Cooke, P., DeArelland, K., Dewar, K., Diaz, J.S., Dodge, S., Farreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission L. Submitted (20-DEC-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Dec 20, 2012 this sequence version replaced gi:17149550. Smit, A.F.A. & Green, P. (1996-1997)	Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission Submitted (29-NoV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 112321) Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chararo, B., Chespel V., Collymore A					
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14 GCCATCTGCAGGGTCCAGGTGATGG 38
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1 (Dases 1 to 439)

Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F., Kvasha,S.M. Podowski,R.M., Matushkin,Y.G., Gyanchandani,A., Muravenko,O.V., Leviteky,V.G., Kolchanov,N.A., Protopopov,A.I., Kashuba,V.I., Kisselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R. Kisselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R. Notlaking sequences: a tool for gene discovery and verifications of the human coordinates.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the human genome Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                   Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre, Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171
                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                     Zabarovsky, E.R.
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PN JP 2001526063-A/9

PD 18-DEC-2001

PF 15-DEC-1998 JP 2000525451

PF 15-DEC-1998 JP 2000525451

PF 15-DEC-1997 US 60/068179,11-SEP-1998 US 60/099840 PI

YI SUN

PC C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P17/02,A61P35/00,

PC A61P39/06,

PC A61P39/06,

PC A61P43/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC

PC G01N39/50,G01N33/68,C12N15/00,A61K37/02,C12N5/00 CC

Strandedness: Double;

CC Topology: Linear;

CC Topology: Linear;

CC SAG:apoptosis sensitivity gene

EVACUATION PROPERTY OF THE P
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3538)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Buck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
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Patent: JP 2001526063-A 9 18-DEC-2001;
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/db_xref="taxon:32644"
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Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, K.J., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, K.J., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, K.J., Delaney, K.Z., Dinh, K.J., Dinh, K., Harl, K., Harl, M., Garner, T., Garza, N., Gill, R., Garner, T., Garza, N., Gill, R., Gabisi, A., Gaoria, A., Garner, T., Garza, N., Gill, R., Garner, T., Garza, N., Garner, J., Martin, R., Jolivet, S., Hamilton, K., Martindale, A., Nolasa, N., Martin, R., Martin, R., Martindale, A., Nolasa, N., Martin, R., Martindale, A., Nolasa, N., Payton, B., Martin, R., Martindale, A., Nolasa, N., Morris, S., Moser, M., Neal, D., Newtson, N., Nguyen, A., Nguyen, N., Nguyen
CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the
                                                                                                                                                                                                                                                                                                    Submitted (28-SEP-2002) Human Genome Sequencing Center, Depa of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
On Jul 30, 2002 this sequence version replaced gi:20976460.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (25-MAY-2002) Human Genome Seq
of Molecular and Human Genetics, Baylor
Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 35638)
                                                                                                                                                                                                                                                                                      gc-help@bcm.tmc.edu
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Baylor Plaza, Houston,
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (24-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Direct Submission
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Direct Submission
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lar and Human Genetics, Baylor College of Medicine, One
aza, Houston, TX 77030, USA
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REFERENCE AUTHORS TITLE JOURNAL

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COMMENT

ANNOTATION OF FEATURES: STSs are identified using ePCR (Genome Res. 7:541-550) searches

Features listing.

of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST

(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the State Lorentzities by Burden. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the State and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:

http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html. Location/Qualifiers

FEATURES

repeat_region misc_feature source repeat_region /rpt_ 3643. complement (6380. complement (6154. /rpt complement (5405. complement (5288.
/rpt_family="L1M complement (4994. complement (3777 complement (2701. complement (2109 complement (1283. complement (3541. complement (2464. complement (2204. .2463) , Tpt /rpt /rpt_family="AluSx" [618. .1906)dz) rpt /rpt rpt_family="AluSx" organism="Homo sapiens" standard name="SHGC-105132" note="overlaps bases 56107. .58001 of clone AC092978" db_xref="taxon:9606" chromosome="3" function="clone overlap" clone="RP11-144C9" .1895 _family="AluSg/x" Lement (5717 family="AluSx"
[ement(5717 lement (2843. _family="(GGGGA)n" family="L1MEc" family="AluSq" family="L1M4"
ement (25.1 family="AluSc" ement(28/) family="L1M4"
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ement(000 family="AluSx" family="AluSg/x type="genomic .6379) .6153) .5287) .5404) .4993) .6394)

repeat_region

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Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnateead, M., Benahmed, F.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Bhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M. L., Davois, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
Rattus norvegicus (Norway rat)
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AC106176
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complement(13819..14^,
/rpt_family="A"
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/rpt_family="AluSp"
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complement(14655...1
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/rpt_family="L2"
11949. .12489
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100.0%; Pred. No. 0.0001
Live 0; Mismatches
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ement(1485)
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COMMENT

Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu ------ Project Information

Center: Baylor Co

College

of Medicine

Web site:

Center project name: GJOH

Center clone name: CH230-20P16

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submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 13, 2003 this sequence version replaced gi:24819215.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projecte/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature table.
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Hollins, B., Howells, S., Hladwin, S.L., Hodgson, A., Hogles, M.,
Jackson, L., Jacob, L., Jiang, H., Johnson, R., Johnson, R.,
Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorensuhewa, L., Loulseged, H., Lozado, R. J., Lu, X., Ma, J.,
Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Margum, A.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
Mawhiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,
Mawhiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,
Maniney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,
Maniney, S., McLeod, M.P., McNeill, T.Z., Mennemayor, J., Moore, S.,
Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Marciney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,
Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L.,
Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L.,
Plazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regiter, M.A., Reigh, R.,
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Shet, H.,
Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shet, H.,
Shetty, J., Shvartsbeyn, A., Sisson, T., Sitter, C.D., Smajs, D.,
Shetty, J., Shvartsbeyn, A., Sisson, T., Sitter, C.D., Smajs, D.,
Shetty, J., Shvartsbeyn, A., Svatek, A., Trejos, Z., Usmani, K.,
Valas, R., Weis, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
Valas, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Williams, G., Willson, R., Wlezzyk, R., Wooden, H., Worley, K.,
Wright, D., Waright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Williams, G., Williams, R., Mu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
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Williams, G., Williams, R., Mu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V
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Worley, K.C.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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-- Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164432
Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davils, C., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Farser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Garday, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamilton, C., Hamilton, C., Hamilton, K., Anderson, N., Hernandez, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 GCCATCTGCAGGGTCCAGGTGATGG 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC098496 245476 bp DNA linear HTG 10-M Rattus norvegicus clone CH230-23C21, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC098496.8 GI:30521845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCATCTGCAGGGTCCAGGTGATGG 164408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 245476)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Consensus quality: 229461 bases at least Q40 Consensus quality: 231714 bases at least Q30 Consensus quality: 231174b bases at least Q20 Estimated insert size: 239075; sum-of-contigs estimation Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236157
237214
237314
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53668 c 53820 g 62326 t
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="CH230-20P16"
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236156: gap of unknown length
237213: contig of 1057 bp in length
237313: gap of unknown length
238330: contig of 1017 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.7%; Score 25; DB 2; L
100.0%; Pred. No. 0.00078;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3931 others
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SOURCE

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Hernandez,R.,-Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,Y., Loudon,P., Longacre,S., Lopez,J.,
Lorensuhewa,L., Louiseged,H., Lozado,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindartne,M., Mahmoud,M., Martinez,E.,
Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
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Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
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Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Sneder, W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shadlers,M., Strong,R., Sutton,A., Systek,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
Wang,Q., Wang,S., Warren,J., Warren,R., Weix,, White,F.,
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Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
Willson,R., Wiles,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
                                                                      AL Submitted (100-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:24819573.
On May 10, 2003 this sequence version replaced gi:24819573.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (24-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 245476) 3 (bases 1 college Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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Genome Center
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TITLE JOURNAL REFERENCE

AUTHORS TITLE JOURNAL

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

Center project name: GHEY

(enter clone name: CH230-23C21

Assembly program; Atlas 3.0;

Consensus quality: 228381 bases at least Q40

(consensus quality: 230024 bases at least Q20

Consensus quality: 231602 bases at least Q20

Estimated insert size: 236545; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu Center: Baylor College of Medicine

----- Project Information

Center code: BCM

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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                   AC118520/c
LOCUS
                                                                                                                                                                                       REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
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Best Local 8
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Muzny, D. Marie, Metzker, M. Lee., Abramzon, S., Adams, C., Alc
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
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Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Ben
Blswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
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Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z.,
                                                                                                                                                                                                                            Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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AC118520.4 GI:25138134
HTG; HTGS_PHASE1; HTGS_I
                                                                                                                                                                                                                                                                                            Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus clone CH230-304J21,
                                                                                                                                                                                                           Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                   AC118520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               be preserved.
                                                                                                                                                                                  (bases 1 to 189541)
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5617
242824
242924
243959
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69231. .103385
/note="clone_boundary
clone_end:Sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         end |
5617
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1 50656 c 50781 g 63728 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="clone_boundary
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|mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .245476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5516: contig of 5516 bp in length
5616: gap of unknown length
242823: contig of 237207 bp in length
242923: gap of unknown length
243958: contig of 1035 bp in length
244058: gap of unknown length
245476: contig of 1418 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence: BH361779"
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Pred. No. 0.00077;
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21, *** SEQUENCING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 245476;
                                                                                                                                                           Adams, C., Alder, J.,
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                                                                                            Benahmed, F.,
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JOURNAL
REFERENCE
AUTHORS
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JOURNAL

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu

Center code: Center: Baylor

ВСМ College

of Medicine

В S

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Egan, A., Bacotto, M., Engene, C., Evans, C.A., Falls, T., Fan, G., Egan, A., Escotto, M., Engene, C., Evans, C.A., Falls, T., Fan, G., Falls, T., Fan, G., Fan, G., Fan, G., Fan, G., Fan, G., Fan, G., Falls, T., Fan, G., Fan, G.
Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 20, 2002 this sequence version replaced gi:23914484.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (18-APR-2002) Human Genome Sequencing Center, Depay of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 189541)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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RESULT 47
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AC139954.3 GI:28626559
HTG; HTGS_PHASE1; HTGS_DRAFT.
Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Brown, M., Barnet, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
                                                                                                                                                                                                               Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                  Rattus norvegicus
                                                                                                                                                                                                                                                                                      Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus clone
                                                                                                                                                                                           Rattus.
                                                                                                                                                                                                                                                                                                                                                                                 unordered pieces.
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NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGACTGTGTTGTGGTCTGGGGAGA 99
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Consensus quality: 173927 bases at least Q40
Consensus quality: 175924 bases at least Q30
Consensus quality: 175952 bases at least Q20
Estimated insert size: 178045; sum-of-contigs estimation
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clone_end:T7
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complement(184170.
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5 188514; gap of unknown length
5 189541; contig of 1027 bp in length.
Location/Qualifiers
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/mol type="genomic DNA"
/db xref="taxon:10116"
/clone="CH230-304J21"
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SEQUENCE, 52
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Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Baves, K., Egan, A., Escotto, M., Bugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, M., Forbes, L., Foster, M., Guevara, M., Gebrergeorgis, B., Geer, K., Gill, R., Grady, M., Gearra, M., Guevara, M., Gunaratne, P., Haaland, M., Hamil, C., Hamilton, C., Hamilton, C., Hanilton, C., Hanil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baylor Plaza, Houston, TX 7/UJU, USA
On Mar 1, 2003 this sequence version replaced gi:28603887
------ Genome Center
Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (27-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (17-FEB-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 208141)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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Consensus quality: 178143 bases at least Q40
Consensus quality: 184319 bases at least Q30
Consensus quality: 188864 bases at least Q20
Estimated insert size: 182136; sum-of-contigs estimation
                                                                                                                                                                                                                             Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye:
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Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
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NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

NOTE: This is a "working draft' sequence. It currently

consists of 52 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
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                15960: gap of 17557; gap of 19168: contig 22819: contig 23818: contig 23818: contig 23818: contig 23818: contig 33243: gap of 18418: contig 34192: contig 34192: contig 34192: contig 34147: gap of 18418: contig 3418: contig 35192: gap of 185192: gap of 185192:
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    B 1 (bases 1 to 243487)

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Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Asbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Bliswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bardwin, N., Bhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Baves, K., Egan, A., Escotto, M., Bugene, C., Evans, C.A., Falls, T., Fan, G., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garrer, T., Garza, M.,
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Rattus norvegicus (Norway rat)
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AC094582
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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of 6901
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of 6379
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of 5075
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of 7337
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of 3976
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Benahmed, F.,

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Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Henlandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hullyk, S., Khan, Z., King, L., Loyez, J., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, Y., Londacere, S., Lopez, J., Liu, J., Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Lorensuhewa, L., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mahshawari, M., Mahindartne, M., Martin, K., Martin, R., Martinez, E., Mangum, B., Mapua, P., Martin, K., Matrin, R., Martinez, E., Mangum, B., Mapua, P., Morris, S., Munidasa, M., Malloy, K., Mangum, A., Mahiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Mangum, A., Mahiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Mangum, A., Mahiney, S., Morris, S., Munidasa, M., Murphy, M., Nair, L., Martinez, E., Morris, S., Munidasa, M., Murphy, M., Nair, L., Martinez, E., Morris, S., Munidasa, M., Murphy, M., Nair, L., Martinez, S., Munidasa, M., Murphy, M., Nair, L., Martinez, S., Murphy, M., Nair, L., Martinez, M., Musinez, M., Resigh, R., Reilly, B., Reilly, M., Rerez, L., Pfannkoch, C., Plage, F., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Shen, H., Shetty, J., Shvat, K., Rose, M., Rose, R., Ruiz, S.J., Shen, H., Shetty, J., Shvat, M., Rose, M., Rose, R., Riggs, F., Riggs, F., Sterle, R., Sosa, J., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trabor, P., Taylor, C., Taylor, T., Thomas, M., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (09-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 9, 2003 this sequence version replaced gi:24818567.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (15-SBP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat Genome Sequencing Consortium.
Direct Submission
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                                                                                                                                             Center project name: GAYK
Center clone name: CH230-4M15
----- Summary Statistics
                                                                                                                                                                                                                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
Assembly program: Atlas;
Consensus quality: 216410 bases at least
Consensus quality: 218103 bases at least
                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Baylor College of Medicine
Center code: BCM
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2 (bases I to 59155)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Birren, B., Linton, L., Bastien, V., Boguslavkiy, L., Boukhgalter, B.,
Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B.,
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
Cooke, P., DeArcellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 59155)
Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapies chromosome 18, clone RP11-352C3
                                                                                                                                                                                                                                                                                                                  AC104983.1 GI:17977361
HTG; HTGS_PHASE0.
Homo sapiens (human)
                                                                                                                                                           Unpublished
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This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by the finished sequence as soon as it is available and the accession number will be preserved.

1 243487: contig of 243487 bp in length.
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/note="clone_boundary
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/mol_type="genomic DNA"
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L. Submitteed 'Jones' A...
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                                                                                                                                                                                                                                                                                                NOTE: This record contains 70 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows
                                                                                                                                                                                                                                                                overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                          be preserved.
                                                                                                                                                                                                                                                                                                                                                        Contact: sequence submissions@genome.wi.mit.edu
----- Project Information
Center project name: L22883
Center clone name: 352_C_3
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AC108040/c
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                                                                                                MO 63108, 1
On Jan 30,
                                                                                                                                                                                                                                                                                                                                            163521 bp DNA linear F
Homo sapiens chromosome 4 clone RP11-210010, WORKING
SEQUENCE, 4 unordered pieces.
AC108040
          Center: Washington University Genome Sequencing Center Center code: WUGSC wite: http://genome.wustl.edu/gsc/index.shtml Contact: submissions@watson.wustl.edu
                                                                                                               Submitted (24-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
22; Conserv
                                                                                                                                                         Direct Submission
                                                                                                                                                                       2 (bases 1 to 163521)
Waterston,R.H.
                                                                                                                                                                                                               The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                        Homo sapiens
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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Project Information
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1: gap of 100 bp
0: contig of 739 bp in length
0: gap of 100 bp
7: contig of 737 bp in length
7: contig of 737 bp in length
7: gap of 100 bp
8: contig of 756 bp in length
8: gap of 100 bp
9: contig of 757 bp in length
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8: gap of 100 bp
8: contig of 760 bp in length
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3: gap of 100 bp in length
9: gap of 100 bp in length
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gap of 100 bp
contig of 725 bp in length
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gap of 100 bp
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80211 CAAGAGGACTGTGTTGTGGTCT 80190
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Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Due; 100% of read
Assembly program: Phrap; version 0.990319
Consensus quality: 162304 bases at least Q40
Consensus quality: 162344 bases at least Q30
Consensus quality: 162529 bases at least Q20
Insert size: 189000; agarose-fp
Insert size: 163221; sum-of-contigs
                                            71
                                                                                          22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality coverage: 8.88 in Q20 bases; agarose-fp Quality coverage: 8.85 in Q20 bases; sum-of-contigs
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                                                                                                               Similarity
                              CAAGAGGACTGTGTTGTGGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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1665
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32426 c 33346 g 46399 t
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1665. .88984
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112803. .163521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                           note="assembly_name:Contig25
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1664: gap of unknown length
88984: contig of 87320 bp in length
89084: gap of unknown length
112702: contig of 236.8 bp in length
112802: gap of unknown length
112802: gap of unknown length
113521: contig of 50719 bp in length
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Minimum DB seq length: 0
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Perfect score:
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Gapop 60.0 , Gapext 60.0
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l: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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32	32	32	32	32	32	32	127	Score		
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754	754	754	342	342	342	224	1140	Query Match Length DB		
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AAX87322	AAX87321	AAX87317	AAD39674	AAH43570	AAA96883	AAX41085	AAX87313	ID		SUMMARIES
Human sensitive to	Human sensitive to	Human sensitive to	Human RING finger	ROC2 coding sequen	Nucleotide sequenc	Human secreted pro	Mouse sensitive to	Description		

4 5	44	43	42	C 41		39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	. 16	15	14	13	12	11	10	9
17	17	17	17	17	17	18	19	19	19	21	21	21	25	25	25	25	29	29	29	29	30	30	32	32	32	32	32	32	32	32	32	32	32	32	32	32
13.4	13.4	13.4	13.4	13.4	13.4	14.2	15.0	15.0	15.0	16.5	16.5	16.5	19.7	19.7	19.7	19.7	22.8	22.8	22.8	22.8	23.6	23.6	25.2	25.2	25.2	25.2	25.2	25.2	25.2	25.2	25.2	25.2	25.2	25.2	25.2	25.2
355	σ	J.	ū	4	w	18	498	498	225	630	596	264	706	441	439	60	1152	754	754	747	754	754	962	836	836	836	836	754	754	754	754	754	754	754	754	754
22	22	22	22	25	23	20																														
ABA69454	ABA56889	2	ABA46329	ABX20540	AAS84630	AAX87337	7	AAL36982	σ	AAL22239	AAL25052	AAL16209	AAX87316	AAC77493	ABZ11414	ABN40537	AAH25847	AAX87319	AAX87318	AAX87315	AAX87329	AAX87320	AAC77504	ABX73660	ABX73201	AAS26319	AAS25860	AAX87314	AAX87331	AAX87330	AAX87328	AAX87327	AAX87326	AAX87325	AAX87324	AAX87323
foetal	foetal	breast		Human GDP-mannose	DNA encoding novel	Human sensitive to	cDNA encoding nove	Human musculoskele	M. capsulatus gene	breast	breast			Human ORFX ORF3048	polynucle	spliced tr	apoptosis	sensitive t	sensitive	sensitive	sensitive	sensitive t	ORFX O	novel	novel	cDNA	cDNA encod	sensitive	sensitive	sensitive	sensitive	sensitive t	Human sensitive to	sensitive t		Human sensitive to

ALIGNMENTS

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RESULT 1
AAXA87313
ID AAXA87313
ID AAXA87313
ID AAXA87313
ID AAXA87
AC AAXA8
AC AAAXA8
AC AAXA8
AC AAXA8
AC AAXA8
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AC AAXA8
AC AAXA8
AC AAX
                                                                                                                                         11-SEP-1998;
19-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAG gene; sensitive to apoptosis; mouse; cancer; tumour; neurodegenerative disease; muscular dystrophy; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX87313 standard; cDNA; 1140 BP.
                                             (WARN ) WARNER LAMBERT CO.
                                                                                                                                                                                                                                                                                            15-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                  01-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9932514-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vulnerary; therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse sensitive to apoptosis (SAG) gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-SEP-1999 (first entry)
                                                                                                                                    98US-0099840-
97US-0068179.
                                                                                                                                                                                                                                                                                            98WO-US26705.
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Best Local
                                                         Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  suggesting a role in carcinogenesis. SAG genes, and mutant SAG genes, can be used to protect cells from apportosis induced by redox reagents. Antisense SAG genes can be used to inhibit the growth of tumour cells. The SAG genes can also be used for the recombinant production of the SAG proteins. The SAG proteins can be used to scaverage oxygen radicals in organisms and to promote wound healing. Additionally, the SAG genes or their complements can be used to promote or inhibit the growth of plant cells (all claimed). The SAG protein is also an ideal molecular target in the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The cDNA was isolated using differential display to identify genes associated with 1,10-phenanthroline (OP)-induced apoptosis in murine tumour lines, and use of an isolated OP-inducible clone to screen a mouse lung cDNA library. The mouse SAG cDNA was used to identify human SAG (see AAX87314). SAG is highly conserved among species. Disruption in yeast was shown to be lethal. SAG deletion mutants (see AAX87315-16) have been identified in human cancer lines,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This is the nucleotide sequence of mouse sensitive to apoptosis (SAG) cDNA, which codes for a novel redox-sensitive, haem-binding protein (see AAY06491) with a zinc RING finger domain that promotes cell growth, protects cells from apoptosis, scavenges oxygen radicals and can be used for the reversion of a tumour phenotype.
WO9906554-A2
                               Homo sapiens
                                                                                                                                                                                   Human secreted
                                                                                                                                                                                                                    18-JUN-1999
                                                                                                                                                                                                                                                     AAX41085
                                                                                                                                                                                                                                                                                  AAX41085 standard; cDNA; 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-430152/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        drugs against neurodegenerative disorders,
                                                                                                                                                                                                                                                                                                                                                                        274
                                                                                                                                                                                                                                                                                                                                                                                                     121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGCTGC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 48-49; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302 A; 224 C; 287 G; 327 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                   ω
                                                                                                                                                                                   EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 127; DB 20;
Pred. No. 2.5e-57;
                                                                                                                                                                                   SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                   ID NO:
                                                                                                                                                                                   297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancers and muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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RESULT 3
AAASS 883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation/differentiation activity, haematopoiesis regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products activity, tumour inhibition activity or other activities.
                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence of human ring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA96883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human secreted proteins, and encode the proteins given in AAY0160 AAY11994 to AAY12260, respectively. The proteins given represent signal peptide and an N-terminal fragment of a secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX40826 to AAX41093 represent 5' expressed sequence tags (ESTs) for human secreted proteins, and encode the proteins given in AAY01602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acids encoding human secreted proteins - obtained from cDNA libraries prepared from kidney, fetal kidney, dystrophic muscle, muscle and heart tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duclert A,
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                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                        tumour;
                                                                                                                                                                                                                                                                                                    cullin
                                                                                                                                                                                                                                                                                                                          ROC1; ROC2;
                                                                                                                                                                                                                                                                                                                                                                                                                                     19-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA96883 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 441; 622pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        f a polypeptide into a membrane, or importing a polypeptide into cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                    dependent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCATCTGCAGGGTCCAGGTGATGGATGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCATCTGCAGGGTCCAGGTGATGGATGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224
                                                                                                                                                                                                                                                                                              cullin; ring finger
ndent ubiquitin ligas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP; 41 A; 60 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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/transl_except=
/transl_except=
/transl_except=
                                                                                                                                                                  Location/Qualifiers
                                                                                  product= "ROC2"
                                                                                                              *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              342
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                                                                                                                                                                                                                                                                                                    ligase;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 G;
     (pos:
                                                                                                                                                                                                                                                                                                 protein; APC11; APC complex; SCF pathway;
se; CDK inhibitor Sic1 degradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                              finger protein ROC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 T;
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     28..30,
34..36,
40..42,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.6e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 224;
        Val)
Ser)
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RESULT 4
AAH43570
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 342 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful for diagnostic and therapeutic purposes, preferably for diagnosing and treating tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes a human ROC2 ring finger protein. The specification also describes human ROC1. ROC1 and ROC2 are similar to APC11, a subunit of the APC complex. The proteins stimulate cullin dependent ubiquitin ligase activity. ROC1 functions in vivo as an essential regulator of CDK inhibitor Sic1 degradation by the SCF (undefined) pathway. ROC proteins are useful for screening bioactive agents that interfere with the binding of ROC proteins with cullin proteins. Pharmaceutical formulations comprising ROC proteins are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acid encoding cullin regulating ring finger proteins, termed as ROC proteins similar to anaphase-promoting complex 11, for therapeutic and diagnostic use
                      03-APR-2000; 2000US-0542497
                                                03-APR-2001; 2001WO-US10906
                                                                                                 WO200175145-A2
                                                                                                                           Unidentified
                                                                                                                                                Assay; ubiquitin ligase; tag1-ubiquitin; E1; E2; ubiquitin activating enzyme; ubiquitin conjugating enzyme; ubiquitin ligase; ubiquitination modulator; ss.
                                                                                                                                                                                                                              07-JAN-2002
                                                                                                                                                                                                                                                        AAH43570;
                                                                                                                                                                                                                                                                                AAH43570 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-647235/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-1999;
22-NOV-1999;
                                                                                                                                                                                                   ROC2 coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-2000; 2000WO-US08592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-OCT-2000
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(RIGE-) RIGEL PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYNC-) UNIV NORTH CAROLINA
                                                                                                                                                                                                                                                                                                                                                151
                                                                                                                                                                                                                                                                                                                                                              14 GCCATCTGCAGGGTCCAGGTGATGGATGCCTG 45
                                                                                                                                                                                                                                                                                                                                                                                                  32;
                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB19161
                                                                                                                                                                                                                                                                                                                                               GCCATCTGCAGGGTCCAGGTGATGCCTG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ohta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fig 2B; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                              (first entry)
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99US-0166927.
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/transl_except=
/transl_except=
                                                                                                                                                                                                                                                                                                                                                                                                                                                     82
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; 84 C; 108 G; 68 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                             25.2%; Score 32; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                 342
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                                                                                                                                                                                                                                                                                 ВP
                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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(pos: 67..69, aa: Lys)
(pos: 109..111, aa: Ala)
                                                                                                                                                                                                                                                                                                                                                                                                             4.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                               E3 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequences given in AAH43568-72 encode proteins which may be used in the method of the invention for assaying ubiquitin ligase activity. The method comprises combining under conditions that favour ubiquitin collagse activity, tag1-ubiquitin, El (ubiquitin activating enzyme), E2 (ubiquitin conjugating enzyme) and E3 (ubiquitin ligase) and measuring the amount of tag1-ubiquitin bound to the E3. The method is useful for assaying ubiquitin ligase activity and ubiquitination enzyme activity assaying ubiquitin the amount of tag1-ubiquitin, the modulator, E1 and tag2-E3 and measuring the amount of tag1-ubiquitin bound to tag2-E3 and activity is measuring the amount of tag1-ubiquitin bound to tag2-E3 or combining tag1-ubiquitin bound to tag2-E3 are an activity is measured to tag1-ubiquitin bound to tag2-E3. Ubiquitin ligase activity is measured collectly, eliminating the need for target proteins and subsequent canalysis such as separating ligated from unligated material in an SDS-PAGE procedure. This allows multi-well array analysis and high combinations of E3 components and E2/E3 combinations without requiring combinations of E3 components and E2/E3 combinations without requiring combinations of E3 components and E2/E3 combinations without requiring combinations of identification of specific target substrates. Ubiquitin is labeled, directly or indirectly and this allows for easy and rapid detection and component of ligated ubiquitin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 32
                                                                                                                        11-APR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ubiquitin ligase; UL; tag1-ubiquitin; E1; ubiquitin-activating enzyme; E2; ubiquitin-conjugating enzyme/ubiquitin carrier protein; E3; human; RING finger protein; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human RING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD39674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD39674 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 342 BP; 82 A; 84 C;
                                                                                                                                                                                                                US2002042083-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conjugating enzyme,
bound to the ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Assaying ubiquitin ubiquitining the second control of the second c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Issakani SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   finger protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 GCCATCTGCAGGGTCCAGGTGATGGATGCCTG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCATCTGCAGGGTCCAGGTGATGGATGCCTG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             finger protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fig 12A; 98pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.2%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Huang J,
                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                          /*tag= a
/product= "Human ROC2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ligase activity for identifying modulators of combining ubiquitin, ubiquitin activating ubiquitin ilgase and measuring amount of ubiquitin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sheung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROC2 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 32; DB 22;
Pred. No. 4.5e-0
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŗ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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03-APR-2001; 2001US-0826312

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RESULT 6
AAX87317
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Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an assay for ubiquitin ligase (UL) activity which comprises incubating tag1-ubiquitin, E1 (ubiquitin-activating enzyme), E2 (ubiquitin-conjugating enzyme/ubiquitin carrier protein) and E3 (UL) and measuring the amount of tag1-ubiquitin bound to E3. The method is particularly used to screen for modulators of UL activity. The present sequence is human RING finger protein, ROC2 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assay for ubiquitin ligase activity, useful for identifying modulators, by measuring binding of labeled ubiquitin to ubiquitin ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAE24621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-488718/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-APR-2000; 2000US-0542497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 12A; 56pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (RIGE-) RIGEL PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 342 BP; 82 A; 84 C;
                                                                                                                                                                                                                    mutation
                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                          Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                        vulnerary; therapy; mutant; ds.
                                                                                                                                                                                                                                                                                                                    SAG gene; sensitive to apoptosis; human; neurodegenerative disease; muscular dystr
                                                                                                                                                                                                                                                                                                                                                     Human sensitive to apoptosis (SAG)
                                                                                                                                                                                                                                                                                                                                                                           27-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                      AAX87317 standard; cDNA; 754 BP
SAG: Sensitive to Apoptosis Gene and related proteins, useful
                      WPI; 1999-430152/36.
P-PSDB; AAY06495.
                                                       aus
                                                                                                 11-SEP-1998;
19-DEC-1997;
                                                                                                                                 15-DEC-1998;
                                                                                                                                                      01-JUL-1999
                                                                                                                                                                            WO9932514-A2
                                                                            (WARN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 GCCATCTGCAGGGTCCAGGTGATGGATGCCTG 45
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                                                                            WARNER LAMBERT CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCATCTGCAGGTCCAGGTGATGGATGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                  98US-0099840.
97US-0068179.
                                                                                                                                  98WO-US26705
                                                                                                                                                                                                                     replace(148,T)
                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                  note= "C50S mutation"
                                                                                                                                                                                                             *tag=
                                                                                                                                                                                                                                  *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sheung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 G; 68 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pray TR;
                                                                                                                                                                                                                                                                                                                                                       gene mutant MM1.
                                                                                                                                                                                                                                                                                                                       dystrophy; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 24;
                                                                                                                                                                                                                                                                                                                                   cancer; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 342;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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RESULT 7
AAX87321
ID AAX8
XX
AC AAX8
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ś
                                                                                                                                                                                                               This is the nucleotide sequence of human sensitive to apoptosis (SAG) mutant gene MM1, which codes for a SAG protein (see AAY06495) (and which the Cys residue at position 50 of the native protein (see AAY06492) is replaced by a Ser residue owing to a mutation of codon 50 from TGC to AGC obtained by site-directed mutagenesis of SAG CDNA. This residue is at a haem binding site of SAG. Single and Cdouble SAG mutants (see AAX87317-31) were made in order to determine 30 cluble sad mutants (see AAX87317-31) were made in order to determine 60 cligomerization. MM1 showed reduced haem binding but unaffected 61 coligomerization. SAG is a novel zinc finger protein that promotes 61 growth, protects cells from apoptosis, scavenges oxygen 62 cradicals and can be used for the reversion of a tumour phenotype. 62 cradicals and can be used for the reversion of a tumour phenotype. 63 creembinant production of SAG genes, and mutant SAG genes, can be used to protect cells from 62 cradicals induced by redox reagents. They can also be used for the recombinant production of SAG proteins, which are molecular targets 62 in the development of drugs against neurodegenerative disorders, 62 cancers and muscle dystrophy, and promoting wound healing.
XRRXPXRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                promoting cell growth and protecting cells against apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 15;
                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                               SAG gene; sensitive to apoptosis; human; cancer; tumc neurodegenerative disease; muscular dystrophy; wound vulnerary; therapy; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX87321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX87321 standard; cDNA; 754 BP.
                                                                                                                                                                                                                                                                                          mutation
                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human sensitive to apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-1999
                                                                                                                                                                                                 01-JUL-1999.
                                                                                                                                                                                                                               WO9932514-A2
           WPI; 1999-430152/36.
P-PSDB; AAY06499.
                                                          Sun Y;
                                                                                                                     11-SEP-1998;
19-DEC-1997;
                                                                                                                                                                   15-DEC-1998;
                                                                                        (WARN ) WARNER LAMBERT CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 GCCATCTGCAGGGTCCAGGTGATGGATGCCTG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         754 BP; 206 A; 155 C; 201 G; 192 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCATCTGCAGGGTCCAGGTGATGCATGCCTG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                        98US-0099840
97US-0068179
                                                                                                                                                                      98WO-US26705
                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                         replace(238,T)
/*tag= b
                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.2%;
                                                                                                                                                                                                                                                               b
"C80S mutation"
                                                                                                                                                                                                                                                                                                               ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SAG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer; tumour;
rophy; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MM5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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RESULT 8
AAX87322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oligomerization. These properties were unaffected by the MM5 mutation. SAG is a novel zinc finger protein that promotes cell growth, protects cells from apoptosis, scavenges oxygen radicals and can be used for the reversion of a tumour phenotype. SAG genes, and mutant SAG genes, can be used to protect cells from apoptosis induced by redox reagents. They can also be used for the recombinant production of SAG proteins, which are molecular targets in the development of drugs against neurodegenerative disorders, cancers and muscle dystrophy, and promoting wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the nucleotide sequence of human sensitive to apoptosis (SAG) mutant gene MM5, which codes for a SAG protein (see AAY06499) in which the Cys residue at position 80 of the native protein (see AAY06492) is replaced by a Ser residue owing to a mutation of codon 80 from TGC to AGC obtained by site-directed mutagenesis of SAG cDNA. This residue is in zinc-ring finger 1 of SAG. Single and double SAG mutants (see AAX87317-31) were made in order to determine the role of each cysteine residue of SAG in haem binding and SAG constraints.
WPI; 1999-430152/36.
P-PSDB; AAY06500.
                                              Sun Y;
                                                                                                                                                                             01-JUL-1999.
                                                                                                                                                                                                                                                                  mutation
                                                                                                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                  SAG gene; sensitive to apoptosis; human; cancer; tumour; neurodegenerative disease; muscular dystrophy; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human sensitive to apoptosis (SAG) gene mutant MM6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX87322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX87322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 754 BP; 206 A; 155 C; 201 G; 192 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAG: Sensitive to Apoptosis Gene and related proteins, useful for promoting cell growth and protecting cells against apoptosis
                                                                                                      11-SEP-1998;
19-DEC-1997;
                                                                                                                                              15-DEC-1998;
                                                                                                                                                                                                       W09932514-A2
                                                                                                                                                                                                                                                                                                                                                                                    vulnerary; therapy; mutant; ds.
                                                                        (WARN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 GCCATCTGCAGGGTCCAGGTGATGGATGCCTG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32;
                                                                          WARNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCATCTGCAGGGTCCAGGTGATGCCTG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                        LAMBERT CO
                                                                                                    98US-0099840
97US-0068179
                                                                                                                                               98WO-US26705
                                                                                                                                                                                                                                                                /*tag= a
replace(244..246,CAT)
                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                      note= "H82K mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA; 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 32;
; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.5e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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RESULT 9
AAX87323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                 Sun
WPI; 1999-430152/36.
                                                                                                                                                                                                    11-SEP-1998;
19-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurodegenerative disease; muscular dystrophy; wound healing; vulnerary; therapy; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAG gene; sensitive to apoptosis; human; cancer; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX87323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX87323 standard; cDNA; 754 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 754 BP; 207 A; 154 C; 201 G; 192 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAG: Sensitive to Apoptosis Gene and related proteins, useful for promoting cell growth and protecting cells against apoptosis
                                                                                                                                                                                                                                                                                                15-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                            WO9932514-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human sensitive to apoptosis (SAG) gene mutant MM7
                                                                                                                                  (WARN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 GCCATCTGCAGGGTCCAGGTGATGGATGCCTG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Page 67-68; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32;
                                                                                                                               WARNER LAMBERT CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                             98US-0099840.
97US-0068179.
                                                                                                                                                                                                                                                                                                98WO-US26705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
replace(253..255,CAC)
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "H85K mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
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P-PSDB; AAY06501

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 754 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               promoting
                                                                                                                                                                                                                                                                                                                                            SAG gene; sensitive to apoptosis; human; cancer; tumour; neurodegenerative disease; muscular dystrophy; wound healing; vulnerary; therapy; mutant; ds.
                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                  27-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX87324 standard; cDNA;
            Sun Y;
                                                                     11-SEP-1998;
19-DEC-1997;
                                                                                                               15-DEC-1998;
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                                                                                                                                                                       WO9932514-A2
                                                                                                                                                                                                                              mutation
                                                                                                                                                                                                                                                                                                  synthetic.
                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                    Human sensitive to apoptosis
                                        (WARN ) WARNER LAMBERT CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCATCTGCAGGGTCCAGGTGATGGATGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCATCTGCAGGGTCCAGGTGATGGATGCCTG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            itive to Apoptosis Gene and related proteins, useful cell growth and protecting cells against apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                     98US-0099840.
97US-0068179.
                                                                                                               98WO-US26705
                                                                                                                                                                                                              replace(262,T)
/*tag= b
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                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.2%;
                                                                                                                                                                                                   "C88S mutation"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                         (SAG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      gene mutant MM8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              related proteins, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 20; 1
4.5e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 754;
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RESULT 11
AAX87325
ID AAX87
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AC AAX87
AC
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human sensitive to apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-SEP-1999
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                                                                                                                                           11-SEP-1998;
19-DEC-1997;
                                                                                                                                                                                                                                               15-DEC-1998;
                                                                                                                                                                                                                                                                                                               01-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vulnerary; therapy; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neurodegenerative disease;
                                                                                                                                                                                                                                                                                                                                                                                   WO9932514-A2
                                                                       (WARN ) WARNER LAMBERT CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY06502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCATCTGCAGGGTCCAGGTGATGCATGCCTG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCATCTGCAGGGTCCAGGTGATGGATGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 754 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.2%; Scilarity 100.0%; For Conservative 0;
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                                                                                                                                           98US-0099840
97US-0068179
                                                                                                                                                                                                                                               98WO-US26705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   replace(295,T)
/*tag= b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    206 A; 155 C; 201 G; 192 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "C99S mutation"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA;
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; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SAG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MM9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Best Local S
Matches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               double SAG mutants (see AAX87317-31) were made in order to determine the role of each cysteine residue of SAG in haem binding and SAG oligomerization. These properties were unaffected by the MM9 mutation. SAG is a novel zinc finger protein that promotes cell growth, protects cells from apoptosis, scavenges oxygen radicals and can be used for the reversion of a tumour phenotype. SAG genes, and mutant SAG genes, can be used to protect cells from apoptosis induced by redox reagents. They can also be used for the recombinant production of SAG proteins, which are molecular targets in the development of drugs against neurodegenerative disorders, cancers and muscle dystrophy, and promoting wound healing.
                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                   mutation
                                                                                                                                                                                                                                                                                                                                                      SAG gene; sensitive to apoptosis; human; cancer; tumour; neurodegenerative disease; muscular dystrophy; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                         Human sensitive to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX87326 standard; cDNA; 754 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is the nucleotide sequence of human sensitive to apoptosis (SAG) mutant gene MM9, which codes for a SAG protein (see AAY06503) in which the Cys residue at position 99 of the native protein (see AAY06492) is replaced by a Ser residue owing to a mutation of codon 99 from TGC to AGC obtained by site-directed mutagenesis of SAG cDNA. This residue is in zinc-ring finger 2 of SAG. Single and double SAG mutants (see AAX87317-31) were made in order to determine
11-SEP-1998;
19-DEC-1997;
                                                                            01-JUL-1999.
                                                                                                       WO9932514-A2
                                                                                                                                                                     mutation
                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                       27-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 754 BP; 206 A; 155 C; 201 G; 192 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 15; Page 72-73; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAG: Sensitive to Apoptosis Gene and related proteins, useful promoting cell growth and protecting cells against apoptosis
                                           15-DEC-1998;
                                                                                                                                                                                                                                                                                                                                        vulnerary; therapy; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-430152/36.
P-PSDB; AAY06503.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCATCTGCAGGGTCCAGGTGATGGATGCCTG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
98US-0099840
97US-0068179
                                             98WO-US26705
                                                                                                                                                   /note= "H85K mutation"
replace(253..255,CAC)
/*tag= c
                                                                                                                                                                                                 replace(244..246,CAT)
/*tag= b
                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                       apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.2%;
100.0%;
                                                                                                                                     "H85K mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32; DB 20;
Pred. No. 4.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                       (SAG)
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                                                                                                                                                                                                                                                                                                                                                                                                     gene mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 754;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                              SAG gene; sensitive to apoptosis; human; cancer; tumour; neurodegenerative disease; muscular dystrophy; wound healing; vulnerary; therapy; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             each cysteine residue of SAG in haem binding and oligomerization. These properties were unaffected by the MM10 mutations. SAG is a novel zinc finger protein that promotes cell growth, protects cells from apoptosis, scavenges oxygen radicals and can be used for the reversion of a tumour phenotype. SAG genes, and mutant SAG genes, can be used to protect cells from apoptosis induced by redox reagents. They can also be used for the recombinant production of SAG proteins, which are molecular targets in the development of drugs against neurodegenerative disorders, cancers and muscle dystrophy, and promoting wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is the nucleotide sequence of human sensitive to apoptosis (SAG) mutant gene MM10, which codes for a SAG protein (see AAY06504) in which the His residues at positions 82 and 85 of the native protein (see AAY06492) are replaced by Lys residues owing to mutations of codons 82 and 85 by site-directed mutagenesis of SAG CDNA. These residues are in zinc-ring fingers 1 and 2 of SAG. SAG mutants (see AAX87317-31) were made in order to determine the role of
11-SEP-1998;
                             15-DEC-1998;
                                                            01-JUL-1999.
                                                                                                                                                       mutation
                                                                                                                                                                                      Cbs
                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                               27-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 754 BP; 208 A; 152 C; 202 G; 192 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAG: Sensitive to Apoptosis Gene and related proteins, useful for promoting cell growth and protecting cells against apoptosis
                                                                                            WO9932514-A2
                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                            Human sensitive to apoptosis (SAG) gene mutant MM11
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX87327 standard; cDNA; 754 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 15; Page 74-75; 84pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAY06504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-430152/36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCATCTGCAGGGTCCAGGTGATGGATGCCTG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCATCTGCAGGGTCCAGGTGATGCATGCCTG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ilarity 100.0%; I Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                               (first entry)
98US-0099840
                             98WO-US26705
                                                                                                                    /*tag= a
replace(190,T)
/*tag= b
/note= "C64S mutation"
                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.5e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 754;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA. This residue is in zinc-ring finger 1 of SAG. Single and double SAG mutants (see AAX67317-31) were made in order to determine the role of each cysteine residue of SAG in haem binding and SAG oligomerization. These properties were unaffected by the MM11 mutation. SAG is a novel zinc finger protein that promotes cell growth, protects cells from apoptosis, scavenges oxygen radicals and can be used for the reversion of a tumour phenotype. SAG genes, and mutant SAG genes, can be used to protect cells from apoptosis induced by redox reagents. They can also be used for the recombinant production of SAG proteins, which are molecular targets in the development of drugs against neurodegenerative disorders, cancers and muscle dystrophy, and promoting wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 15; Page 76; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAG: Sensitive to Apoptosis Gene and related proteins, useful promoting cell growth and protecting cells against apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-430152/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sun Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 754 BP; 206 A; 155 C; 201 G; 192 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (WARN ) WARNER LAMBERT CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is the nucleotide sequence of human sensitive to apoptosis (sac) mutant gene MM11, which codes for a SAG protein (see AAY06505)
                                                                                                                                                                                                                                                         vulnerary; therapy; mutant; ds.
                                                                                                                                                                                                                                                                               SAG gene; sensitive to apoptosis; human; neurodegenerative disease; muscular dysti
                                                                                                                                                                                                                                                                                                                              Human sensitive to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SAG) mutant gene MM11, which codes for a SAG protein (see AAY0650: in which the Cys residue at position 64 of the native protein (see AAY06492) is replaced by a Ser residue owing to a mutation of code 64 from TGT to AGC obtained by site-directed mutagenesis of SAG
              15-DEC-1998;
                                            01-JUL-1999.
                                                                           WO9932514-A2
                                                                                                                                       mutation
                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                           27-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                        AAX87328 standard; cDNA; 754 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCATCTGCAGGGTCCAGGTGATGCATGCCTG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                           (first entry)
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              98WO-US26705
                                                                                                                /*tag= a
replace(217,T)
/*tag= b
/*tag= b
                                                                                                                                                                      Location/Qualifiers
1..342
                                                                                                        /*tag= b
/note= "C73S mutation"
                                                                                                                                                                                                                                                                                                                            apoptosis (SAG) gene mutant MM12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.2%; Score 32; DB 20; 100.0%; Pred. No. 4.5e-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 754;
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RESULT 15
AAX87330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA. This residue is in a protease inhibitor motif of SAG. Single and double SAG mutants (see AAX87317-31) were made to determine the role of each cysteine residue of SAG in haem binding and SAG oligomerization. These properties were unaffected by the MM12 mutation. SAG is a novel zinc finger protein that promotes cell growth, protects cells from appottosis, scavenges oxygen radicals and can be used for the reversion of a tumour phenotype. SAG genes, and mutant SAG genes, can be used to protect cells from appottosis induced by redox reagents. They can also be used for the recombinant production of SAG proteins, which are molecular targets in the development of drugs against neurodegenerative disorders, cancers and muscle dystrophy, and promoting wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the nucleotide sequence of human sensitive to apoptosis (SAG) mutant gene MM12, which codes for a SAG protein (see AAY06506) in which the Cys residue at position 73 of the native protein (see AAY06492) is replaced by a Ser residue owing to a mutation of codon 73 from TGT to AGC obtained by site-directed mutagenesis of SAG 73 from TGT to AGC obtained by site-directed mutagenesis of SAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAG: Sensitive to Apoptosis Gene and related proteins, useful promoting cell growth and protecting cells against apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-SEP-1998;
19-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-430152/36
                                                                                                                                                                                                                        SAG gene; sensitive to apoptosis; human; cancer; tumour; neurodegenerative disease; muscular dystrophy; wound healing; vulnerary; therapy; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 754 BP; 206 A; 155 C; 201 G; 192 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 15; Page 77-78; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAY06506.
                                                                                                                                                                         Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                  Human sensitive to apoptosis (SAG) gene mutant MM14.
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                                                                                                                                                                                                                                                                                                                                                                       AAX87330;
                                                                                                                                                                                                                                                                                                                                                                                                         AAX87330 standard; cDNA; 754
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                                                                                  mutation
                                                                                                                     CDS
                               mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 GCCATCTGCAGGGTCCAGGTGATGGATGCCTG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCATCTGCAGGTCCAGGTGATGGATGCCTG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0099840.
97US-0068179.
                                                                 replace(295,C)
/*tag= b
                               replace(304,C)
                                              /*tag= b
/note= "C99S mutation"
                                                                                                                                      location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.2%;
"C102S mutation"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 32; DB 20;
Pred. No. 4.5e-0;
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WO9932514-A2

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RESULT 16
AAX87331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SAG) mutant gene MM14, which codes for a SAG protein (see AAY06508)

(in which the Cys residues at positions 99 and 102 of the native protein (see AAY06492) are replaced by Ser residues owing to mutations of codons 99 and 102 through site-directed mutagenesis of SAG cDNA. These residues are in zinc ring finger 2 of SAG. Single double SAG mutants (see AAX87317-31) were made in order to determine the role of each cysteine residue of SAG in haem binding and SAG oligomerization was observed, indicating that these residues are important for intermolecular disulfide bond formation. SAG is a novel zinc finger protein that promotes cell growth, protects cells from apoptosis, scavenges oxygen radicals and can be used for the reversion of a tumour phenotype. SAG genes, and mutant SAG genes, can be used to protect cells from apoptosis, which are molecular targets in the development of durings against neurodegenerative disorders, cancers and muscle
                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                  SAG gene; sensitive neurodegenerative
                            mutation
                                                                                                                                                                                                Human sensitive to apoptosis
                                                                                                                                                                                                                                                                                    AAX87331 standard; cDNA; 754 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 754 BP; 207 A; 155 C; 201 G; 191 T; 0
                                                                                                                                         vulnerary; therapy;
                                                                                                                                                                                                                              27-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dystrophy, and promoting wound healing.
                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is the nucleotide sequence of human sensitive to apoptosis
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19-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                        151 GCCATCTGCAGGTCCAGGTGATGGATGCCTG 182
                                                                                                                                                                                                                                                                                                                                                                                      14
                                                                                                                                                                                                                                                                                                                                                                                                                  32;
                                                                                                                                                                                                                                                                                                                                                                                  GCCATCTGCAGGGTCCAGGTGATGGATGCCTG 45
                                                                                                                                                                  sensitive to apoptosis; human; cancer; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 81; 84pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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97US-0068179.
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           replace(139,C)
/*tag= b
                                        /*tag=
                                                                   Location/Qualifiers
'note= "C47S mutation"
                                                                                                                                                      disease;
                                                                                                                                       mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                              25.2%; Score 32; DB 20; 100.0%; Pred. No. 4.5e-0
                                                                                                                                                      muscular
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                                                                                                                                                                                                (SAG)
                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                              gene mutant MM15
                                                                                                                                                      dystrophy; wound healing;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 754;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
             WO9932514-A2
                                                                                                          Homo sapiens
                                                                                                                                        vulnerary; therapy; ds.
                                                                                                                                                       SAG gene; sensitive to apop neurodegenerative disease;
                                                                                                                                                                                                       Human sensitive to apoptosis (SAG) gene.
                                                                                                                                                                                                                                        27-SEP-1999
                                                                                                                                                                                                                                                                        AAX87314;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 754 BP; 206 A; 155 C; 201 G; 192 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 15; Page 82-83; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAG: Sensitive to Apoptosis Gene and promoting cell growth and protecting
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P-PSDB; AAY06509.
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                                                                                                                                                                                                                                                                                                                                                                                                            14 GCCATCTGCAGGGTCCAGGTGATGGATGCCTG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                     32;
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                                                                                                                                                                        sensitive to apoptosis; human; cancer; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ilarity 100.0%; | Conservative 0;
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                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.2%; Score 32;
100.0%; Pred. No.
                                                                                                                                                         muscular dystrophy; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 754;
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RESULT 18
AAS25860
ID AAS25
XX AAS25
AC AAS25
XX O7-NC
DT O7-NC
XX Humar
XX Humar
KW Cytos
KW neurc
KW vulne
KW hype;
KW cere)
KW cerel
KW cerel
KW cerel
XW cerel
XW corn
XX Humar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is the nucleotide sequence of human sensitive to apoptosis (SAG) cDNA, which codes for a novel redox-sensitive, haem-binding CC (SAG) cDNA, which codes for a novel redox-sensitive, haem-binding CC protein (see AAY06492) with a zinc RING finger domain that promotes ccell growth, protects cells from apoptosis, scavenges oxygen CC radicals and can be used for the reversion of a tumour phenotype. CC The cDNA was isolated from a Hela cell CDNA library using mouse CC SAG cDNA (see AAX87311) as probe. SAG is highly conserved among CC secies. Disruption in yeast was shown to be lethal. SAG deletion CC mutants (see AAX87315-16) have been identified in human cancer lines, cc suggesting a role in carcinogenesis. SAG genes, and mutant SAG CC genes, can be used to protect cells from apoptosis induced by redox CC genes, can be used to protect cells from apoptosis induced by redox CC tumour cells. The SAG genes can also be used for the recombinant CC production of the SAG proteins. The SAG proteins can be used to scavenge oxygen radicals in organisms and to promote wound healing. C Additionally, the SAG genes or their complements can be used to protein is also an ideal molecular target in the development of constant natural constant and mutant and mutant?
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P-PSDB; AAY06492.
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                                                                                                     Human, immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 754 BP;
                                       cerebrovascular disorder; cerebral ischaemia; angiogenesis; cerebrovascular disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
                                                                                         vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest;
                                                                                                                                                                      Human cDNA encoding a novel secreted protein,
                                                                                                                                                                                                07-NOV-2001
                                                                                                                                                                                                                                                  AAS25860 standard; cDNA; 836 BP
               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sensitive to Apoptosis Gene and related proteins, useful oting cell growth and protecting cells against apoptosis
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                                                                                                                                                                                                                                                                                                                                           14
                                                                                                                                                                                                                                                                                                                                                                    32;
                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                 GCCATCTGCAGGGTCCAGGTGATGGATGCCTG 182
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ilarity 100.0%;
Conservative
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97US-0068179.
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                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                  Score 32;
Pred. No.
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                                                                                                                                                                         Seq ID 39.
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2000US-0234273.

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Ruben SM;
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RESULT 19
AAS26319
ID AAS26
XX AAS26
XX D7 NOT-NO
XX Humar
XX Cereb
KW hypei
KW hypei
KW cereb
KW nervo
KW cereb
KW hypei
KW cereb
KW homo
XX Homo

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Chyperproliferative disorders e.g. neoplasms of the breast or liver,

cc cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders

Cc e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.

Alzheimer's disease, infections caused by bacteria, viruses and fungi

Cc and ocular disorders e.g. corneal infection, and many other

Cc disorders listed in the specification. The polypeptides can also

Cc be used to aid wound healing and epithelial cell proliferation, to

Cc prevent skin aging due to sumburn, to maintain organs before

Cc transplantation, for supporting cell culture of primary tissues, to

Cc regenerate tissues and in chemotaxis. The polypeptides can also be used

Cc as a food additive or preservative to increase or decrease storage

Cc as a food additive or preservative to increase or decrease storage

Cc apabilities, fat content, lipid, protein, carbohydrate, vittamins,

Cc minerals, cofactors and other nutritional components. The present
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Best Local S
Matches 32
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                                                                                                                                                                                                                                                                                                                                                       hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosing, used as foo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective; antibacterial; virucide; fungicide; vulnerary; secreted protein; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS26319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions
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P-PSDB; AAU15873.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; immunosuppressive; antiarthritic; ss; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cDNA encoding a novel secreted protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-NOV-2001
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                                                                                                                                                                                                                                                                                                                        ageing;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity 32; Conserv
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                                                                                                                                                                                                                                                                                                                                   additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA; 836
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31-JAN-2000; 2000US-0179065 17-JAN-2001; 2001WO-US01341 02-AUG-2001 WO200155322-A2 Homo sapiens

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24-FEB-2000)
224-FEB-2000)
224-FEB-2000)
224-FEB-2000)
11-MAR-2000)
11-MAR-2000)
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29-JUN-2000)
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2000US-0184664

2000US-0186350

2000US-018974

2000US-0199173

2000US-02198123

2000US-020467

2000US-0214886

2000US-0214886

2000US-0215135

2000US-0216847

2000US-02151880

2000US-0216847

2000US-0216847
  2000US-0217496.
2000US-021964.
2000US-0229641.
2000US-0225214.
2000US-0225214.
2000US-0225266.
2000US-0225267.
2000US-0225757.
2000US-0225759.
2000US-0225768.
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2000US-0225789.
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2000US-023949.
2000US-0231244.
2000US-0231244.
2000US-0231244.
2000US-0231413.
2000US-0231413.
2000US-0231413.
2000US-0231441.

             02-OCT-2000; 02-OC
           New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives -
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P-PSDB; AAU16332.
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2000US-0240960.
2000US-0241221.
2000US-0241785.
2000US-0241786.
2000US-0241787.
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2000US-0241809.
2000US-0241809.
2000US-0244617.
2000US-0246476.
2000US-0246476.
2000US-0246524.
2000US-0246524.
2000US-0246526.
2000US-0246526.
2000US-0246526.
2000US-0246609.
2000US-0246611.
2000US-0246611.
2000US-0246613.
2000US-0249210.
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2000US-0249216.
2000US-0249217.
2000US-0249218.
2000US-0249219.
2000US-0251186.
2000US-0251186.
2000US-0251188.
2000US-0251188.
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2000US-0251988.
2000US-02511989.
2000US-0251999.
2000US-0251999.
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2000US-0237039.
2000US-0237040.
2000US-0239935.
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Claim 1;

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c immunosorbant assays (ELISA). Disorders which are diagnosed or treated
c include autoimmune diseases e.g. rheumatoid arthritis,
c hyperproliferative disorders e.g. rheumatoid arthritis,
c reprovance a control isorders e.g. rheumatoid arthritis,
c e.g. cerebroal isorders e.g. cardiac arrest, cerebrovascular disorders
c e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.
c e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.
c Alzheimer's disease, infections caused by bacteria, viruses and fungi
and coular disorders e.g. corneal infection, and many other
c disorders listed in the specification. The polypeptides can also
be used to aid wound healing and epithelial cell proliferation, to
c prevent skin aging due to sunburn, to maintain organs before
c transplantation, for supporting cell culture of primary tissues, to
c egenerate tissues and in chemotaxis. The polypeptides can also be used
c as a food additive or preservative to increase storage
c exchange a food additive or preservative to increase storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 32
31.JAN-2000

04.FEB-2000

28.JUN-2000

07.JUL-2000

07.JUL-2000

11.JUL-2000

11.JUL-2000

14.JUL-2000

26.JUL-2000

26.JUL-2000
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                                                                                                                                                                                                                                                US2002132753-A1
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                                                                                                                                                                                17-JAN-2001;
                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                 haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABX73201 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence encodes a novel secreted protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  minerals,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ies, fat content, lipid, protein, carbohydrate, vitamins, cofactors and other nutritional components. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                polynucleotide
               2000US-180628P.

2000US-214886P.

2000US-216647P.

2000US-21880P.

2000US-217487P.

2000US-217487P.

2000US-217487P.

2000US-218290P.

2000US-218290P.
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                                                                                                                                                                                                                                                                                                                 ar; nephrotropic; cyt-
antiarteriosclerotic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
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100.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                              cytostatic; antiallergic; thrombolytic;
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CC The invention relates to human novel polypeptides and their associated CC polynucleotides. The polypeptides and polynucleotides are useful in gene CC therapy for treating, inhibiting or preventing neural disorders, immune CC system disorders (e.g. systemic lupus erythematosus, rheumatoid CC arthritis and multiple sclerosis), muscular disorders, respiratory CC diseases (e.g. nasal vestibulitis, nasal polyps and sinusitis), CC reproductive disorders, gastrointestinal disorders, pulmonary disorders, CC cardiovascular disorders (e.g. congenital heart defects, Ebstein's CC anomaly and hypoplastic left heart syndrome), renal disorders (e.g. acute (e.g. Hodgkin's disease and leukaemia), inflammatory diseases (e.g. CC (e.g. Hodgkin's disease and leukaemia), inflammatory diseases (e.g. conditions (e.g. asthma), blood related disorders (e.g. thrombosis, conditions (e.g. asthma), blood related disorders (e.g. thrombosis, conditions ABX73173-ABX74167 represent human novel polynucleotides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-SEP-2000;
29-SEP-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
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21-SEP-2000;
25-SEP-2000;
27-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
                                                                                                                                                                                                                                                      New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or renal disorders -
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P-PSDB; ABU54941.
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(RUBE/)
(BARA/)
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BARASH
                                                                                                                                                                                                                          SEQ ID NO 39; 402pp; English.
                                                                                                                                                                                                                                                                                                                                                               Ruben SM,
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2000US-22959P.
2000US-22959P.
2000US-23413P.
2000US-234274P.
2000US-23497P.
2000US-234397P.
2000US-236387P.
2000US-236367P.
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2000US-236370P.
2000US-237039P.
2000US-23703P.
2000US-23703P.
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2000US-237040P.
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RESULT 21
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ID ABX7
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Best Local S
Matches 32
14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
12-AUG-2000;
22-AUG-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hyperproliferative disorder; inflammatory disease; allergic reaction; blood related disorder; cancer; immunosuppressive; antiinflammatory; cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic; haemostatic; antiarteriosclerotic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCATCTGCAGGGTCCAGGTGATGGATGCCTG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCATCTGCAGGGTCCAGGTGATGGATGCCTG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.2%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polynucleotide #488.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP;
                                              2000US-220963P.
2000US-22451BP.
2000US-22451PP.
2000US-225267P.
2000US-225268P.
2000US-225758P.
2000US-225758P.
2000US-225758P.
2000US-225758P.
2000US-225758P.
2000US-2259343P.
2000US-229343P.
2000US-229343P.
2000US-229343P.
2000US-229343P.
2000US-229343P.
2000US-235337P.
2000US-235334P.
2000US-235334P.
2000US-23427P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-214886P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; 209 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 25; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            renal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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RESULT 22
AAC77504
ID AAC77

standard;

cDNA;

0

X S X F X B X B X B X

Human ORFX 08-FEB-2001 AAC77504; AAC77504

ORF3059 polynucleotide

sequence

SEQ ID

NO:6117.

(first entry)

Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant

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                                                                                                                                                                                                                    The invention relates to human novel polypeptides and their associated polynucleotides. The polypeptides and polynucleotides are useful in gene conterable for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. systemic lupus erythematosus, rheumatoid carthritis and multiple sclerosis), muscular disorders, respiratory conferences (e.g. nesal vestibulitis, nasal polyps and sinusitis), cardiovascular disorders (e.g. congenital heart defects, Ebstein's canomaly and hypoplastic left heart syndrome), renal disorders (e.g. canomaly and hypoplastic left heart syndrome), renal disorders (e.g. cliney failure and end-stage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and leukaemia), inflammatory diseases (e.g. conditions (e.g. sathma), blood related disorders (e.g. thrombosis, conditions) (e.g. sathma), blood related disorders (e.g. thrombosis, conditions) (e.g. sathma), blood related disorders (e.g. sathma), blood related diso
                                                                               Matches
                                                                                                 Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-SEP-2000;
02-CCT-2000;
02-CCT-2000;
02-CCT-2000;
02-CCT-2000;
02-CCT-2000;
02-CCT-2000;
20-CCT-2000;
20-CCT-2000;
20-CCT-2000;
11-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 200
P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ROSE/)
(RUBE/)
(BARA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 498; 402pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cardiovascular or renal disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2003-147444/14.
DB; ABU55400.
219
                                       14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ROSEN C A.
) RUBEN S M.
) BARASH S C.
                                                                                 32;
                                                                                                     Similarity
                                                                                                                                                                   836
                        GCCATCTGCAGGGTCCAGGTGATGGATGCCTG
GCCATCTGCAGGGTCCAGGTGATGGATGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-237039P
2000US-237040P
2000US-239935P
2000US-240960P
2000US-241785P
2000US-24169P
2000US-244617P
2000US-244617P
2000US-249299P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-236370P.
2000US-236802P.
2000US-237037P.
2000US-237038P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-251856P.
2000US-251868P.
2000US-251869P.
                                                                               25.2%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                   ВP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O
                                                                                                                                                                 224 A; 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barash
                                                                                                   Score 32;
; Pred. No.
                                                                                 0;
                                                                                                                                                                 C; 221 G; 211 T; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SC;
                                                                                    Mismatches
                                                                                                                              DB 25;
                                                                                                        4.5e-07;
                                            45
                                                                                                                                                                        other;
                                                                                                                           Length 836;
                                                                                      Indels
                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                               (e.g. acute
                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                            disorders
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                                                                                    Query Match
Best Local Similarity
Matches 32; Conserv
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                                                                                                                                                                                                                                                                     antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellicus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allerdies, anlestic anaemia, burns, wounds, bone and cartilage demane
                                                                                                                                                                                                              allergies, aplastic anaemia, burns, wounds, bone and cartilage damage nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidabetic; hypotensive; dermatological; immunosuppressive; antidabetic; hypotensive; dermatological; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 5300; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-1999; 99US-0127607
02-APR-1999; 99US-0127636
05-APR-1999; 99US-0127728
30-MAR-2000; 2000US-0540763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000; 2000WO-US08621.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000-602362/57.
202 GCCATCTGCAGGGTCCAGGTGATGGATGCCTG 233
                                           14
                             GCCATCTGCAGGGTCCAGGTGATGGATGCCTG 45
                                                                                                                                                                         962 BP;
                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0127607.
99US-0127636.
99US-0127728.
                                                                                                                                                                       265 A;
                                                                                                       25.2%; Score 32; DB 21; 100.0%; Pred. No. 4.5e-07
                                                                                                                                                                         204 C; 243
                                                                                  <u>.</u>
                                                                                    Mismatches
                                                                                                                                                                         G; 250 T; 0
                                                                                                         .5e-07;
                                                                                                                                                                         other;
                                                                                                                              Length 962;
                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 frame
                                                                                  0,
                                                                                  Gaps
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                                                                                                                   쏬봈
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                        Query Match
Best Local
                                                                                                                                             SAG genes, and mutant SAG genes, can be used to protect cells from apoptosis induced by redox reagents. They can also be used for the recombinant production of SAG proteins, which are molecular targets in the development of drugs against neurodegenerative disorders, cancers and muscle dystrophy, and promoting wound healing.
                                                                                                                                                                                                                     double SAG mutants (see AAX87317-31) were made in order to determine the role of each cysteine residue of SAG in haem binding and SAG oligomerization. These properties were unaffected by the MM4 mutation. SAG is a novel zinc finger protein that promotes cell growth, protects cells from apoptosis, scavenges oxygen radicals and can be used for the reversion of a tumour phenotype.
                                                                                                                                                                                                                                                                                                            This is the nucleotide sequence of human sensitive to apoptosis (SAG) mutant gene MM4, which codes for a SAG protein (see AAY06498) in which the Cys residue at position of the native protein (see AAY06492) is replaced by a Ser residue owing to a mutation of codon 50 from TGC to AGC obtained by site-directed mutagenesis of SAG cDNA. This residue is at zinc-ring finger 1 of SAG. Single and
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAG: Sensitive to Apoptosis Gene and related proteins, useful for promoting cell growth and protecting cells against apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAG gene; sensitive to apoptosis; human; cancer; tumour; neurodegenerative disease; muscular dystrophy; wound healing;
                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 15; Page 64-65; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAY06498.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-430152/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sun Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-SEP-1998;
19-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vulnerary; therapy; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human sensitive to apoptosis (SAG) gene mutant MM4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9932514-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX87320 standard; cDNA; 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (WARN )
                                                                      Local Similarity
151
                 14 GCCATCTGCAGGGTCCAGGTGATGGATGCC 43
                                                         30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WARNER LAMBERT CO
                                                                                                                  754 BP; 206 A; 155 C; 201 G; 192 T; 0 other;
                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0099840
97US-0068179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-US26705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          replace(181,T)
/*tag= b
/note= "C61S mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                      23.6%;
                                                         0
                                                        Score 30; DB; Pred. No. 5.2
                                                                      DB 20; I
180
                                                                                    Length
                                                         0
                                                        Gaps
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RESULT 23 AAX87320

AAX87329

AAX87329 standard; cDNA; 754 BP

27-SEP-1999 AAX87329;

(first entry)

SAG gene; sensitive to apoptosis; human; cancer; tumour; Human sensitive to apoptosis (SAG) gene mutant MM13.

neurodegenerative disease; muscular dystrophy; wound

Homo sapiens.

Synthetic.

mutation

replace(181,T)
/*tag= b
/note= "C61S mutation"

mutation

replace(190,T) /*tag= c

/note= "C64S mutation"

WO9932514-A2

Key

Location/Qualifiers

vulnerary; therapy; mutant; ds.

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151

180

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                                                                                                                                       This is the nucleotide sequence of human sensitive to apoptosis (SAG) mutant gene MM13, which codes for a SAG protein (see AAY06507) CC (in which the Cys residues at positions 61 and 64 of the native protein (see AAY06492) are replaced by Ser residues owing to grotein (see AAY06492) are replaced by Ser residues owing to commutations of codons 61 and 64 through site-directed mutagenesis of CC (SAG CDNA. These residues are in zinc ring finger 1 of SAG. Single CSAG CDNA. These residues are in zinc ring finger 1 of SAG. Single CO (SAG CDNA. These residues are in zinc ring finger to determine the role of each cysteine residue of SAG in haem binding and SAG CD (somerization. MM13 showed greatly reduced haem binding (and a CC oligomerization. MM13 showed greatly reduced haem binding (and a CC of company) but oligomerization was unaffected. SAG is correspond for finger protein that promotes cell growth, protects cells from apoptosis, scavenges oxygen radicals and can be used for the C from apoptosis, scavenges oxygen radicals and can be used for the century production of the used for the recombinant production of C reagents. They can also be used for the development of C sAG proteins, which are molecular targets in the development of darugs against neurodegenerative disorders, cancers and muscle
                                Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-SEP-1998;
19-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAG: Sensitive to Apoptosis Gene and related proteins, useful for promoting cell growth and protecting cells against apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-430152/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (WARN ) WARNER LAMBERT CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 15; Page 79-80; 84pp; English.
                                                                                               Sequence
   14 GCCATCTGCAGGGTCCAGGTGATGGATGCC 43
                                                                                               754 BP; 207 A; 155 C; 201 G; 191 T; 0 other;
                                                                                                                             and promoting wound healing.
                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0099840.
97US-0068179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US26705
                                                    100.0%;
                                                                  23.6%;
                                     0
                                                    Score 30;
Pred. No.
                                     Mismatches
                                                    DB 20; I
                                                                     Length 754;
                                        Indels
                                        0
                                          Gaps
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0

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71 CAAGAGGACTGTGTTGTGGTCTGGGGAGA 99

Matches

Similarity

22.8%; Score 29; 100.0%; Pred. No.

DB 20; . 1.7e-05;

Length 747; Indels

0,

Gaps

0

Conservative

0

Mismatches

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RESULT 25
AAX87315
ID AAX8736
ID AAX8736
XX AAX87
XX AAX8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX87315 standard; cDNA; 747
                                                                                              in SAG RNA, but not in genomic DNA. It suggests a possible role for SAG in human carcinogenesis. SAG genes, and mutant SAG genes, can be used to protect cells from apoptosis induced by redox reagents. Antisense SAG genes can be used to inhibit the growth of tumour cells. The SAG genes can also be used for the recombinant tumour cells. The SAG genes can also be used for the recombinant production of the SAG proteins. The SAG proteins can be used to scavenge oxygen radicals in organisms and to promote wound healing. Additionally the SAG genes or their complements can be used to promote or inhibit the growth of plant cells (all claimed). The SAG protein is also an ideal molecular target in the development of drugs against neurodegenerative disorders, cancers and muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is the nucleotide sequence of deletion mutant 1 of the novel human sensitive to apoptosis gene SAG (see also AAX87314). The cDNJ was obtained by PCR amplification of RNA isolated from DLD-1 colon carcinoma cells (ATCC CCL 221). It contains a 7 bp deletion compared with native SAG, starting at nucleotide 170 of the coding region that codes for a potential haem binding site. The frame shift deletion abolishes the downstream zinc finger in the resulting protein (see AAY06493). The mutation was detected by PCR resulting protein (see AAY06493).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAG gene; sensitive to apoptosis; human; cancer; tumour; neurodegenerative disease; muscular dystrophy; wound hea ....lorszy. thorarv. mutant; colon carcinoma; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human sensitive to apoptosis (SAG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAG: Sensitive to Apoptosis Gene and related proteins, useful promoting cell growth and protecting cells against apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sun Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-SEP-1998;
19-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9932514-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 15; Page 54-55; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAY06493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-430152/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (WARN ) WARNER LAMBERT CO
   Sequence 747
                                                                                                                                                                                                                                                                                                                                                                                                                                      resulting protein (see AAY06493).
                                                                     dystrophy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
      BP; 204 A; 155
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97US-0068179
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/*tag=
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      C; 197 G; 191 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
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                    other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA
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201

CAAGAGGACTGTGTTGTGGTCTGGGGAGA 229

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RESULT 26
AAX87318
Query Match
Best Local Similarity
Matches 29; Conserv
                                                                            oligomerization. These properties were unaffected by the MM2 mutation. SAG is a novel zinc finger protein that promotes cell growth, protects cells from apoptosis, scavenges oxygen radicals and can be used for the reversion of a tumour phenotype. SAG genes, and mutant SAG genes, can be used to protect cells from apoptosis induced by redox reagents. They can also be used for the recombinant production of SAG proteins, which are molecular targets in the development of drugs against neurodegenerative disorders, cancers and muscle dystrophy, and promoting wound healing.
                                                                                                                                                                                                           This is the nucleotide sequence of human sensitive to apoptosis (SAG) mutant gene MM2, which codes for a SAG protein (see AAY06496) in which the Cys residue at position 53 of the native protein (see AAY06492) is replaced by a Ser residue owing to a mutation of codon 50 from TGC to AGC obtained by site-directed mutagenesis of SAG CDNA. This residue is at a haem binding site of SAG. Single and double SAG mutantes (see AAX87317-31) were made in order to determine the role of each cysteine residue of SAG in haem binding and SAG oligomerization. These properties were unaffected by the MM2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAG gene; sensitive to apoptosis; human; cancer; tumour; neurodegenerative disease; muscular dystrophy; wound healing;
                                                                                                                                                                                                                                                                                                                                                                         Claim 15; Page 60-61; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                      promoting cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-SEP-1998;
19-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vulnerary; therapy; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human sensitive to apoptosis (SAG) gene mutant MM2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (WARN ) WARNER LAMBERT CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                    Sensitive to Apoptosis Gene and related proteins, useful oting cell growth and protecting cells against apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1999-430152/36
                                                            754
                                                          B₽;
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97US-0068179.
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                                                            206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "C53S mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       replace (157, T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
             22.8%; Score 29; 100.0%; Pred. No.
                                                          A; 155 C; 201
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                                                        G; 192 T; 0 other;
                             DB 20;
                           Length 754;
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Conservative

0

Mismatches

Indels

0

Gaps

0

Sequence 754 BP; 207 A; 155 C;

201 G; 191 T; 0 other;

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RESULT 27
AAX87319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Σg
                                       This is the nucleotide sequence of human sensitive to apoptosis (SAG) mutant gene MMJ, which codes for a SAG protein (see AAY06497) in which the Cys residues at positions 50 and 53 of the native protein (see AAY06492) are replaced by Ser residues owing to mutations of codons 50 and 53 from TGC to AGC Obtained by site-directed mutagenesis of SAG cDMA. These residues are at a haem binding site of SAG. Single and double SAG mutants (see AAX87317-31) were made in order to determine the role of each cysteine residue of SAG in haem binding and SAG oligomerization. MM3 showed greatly reduced haem binding and SAG oligomerization. MM3 showed greatly reduced haem binding and SAG oligomerization was unaffected. SAG is a novel zinc finger protein that promotes cell growth, protects cells from apoptosis, scavenges oxygen radicals and can be used for the reversion of a tumour phenotype. SAG genes, and mutant SAG genes, can be used to protect cells from apoptosis induced by redox reagents. They can also be used for the development of SAG proteins, which are molecular targets in the development of durings against neurodegenerative disorders, cancers and muscle
                                                                                                                                                                                                                                                                                                                                                                          SAG: Sensitive to Apoptosis Gene and promoting cell growth and protecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-SEP-1999
                             dystrophy, and promoting wound healing.
                                                                                                                                                                                                                                                                                                                                           Claim 15; Page 62-63; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-430152/36.
P-PSDB; AAY06497.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sun Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vulnerary; therapy; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human sensitive to apoptosis (SAG) gene mutant MM3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX87319 standard; cDNA; 754
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19-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neurodegenerative disease; muscular dystrophy; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAG gene; sensitive to apoptosis; human; cancer; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (WARN ) WARNER LAMBERT CO
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97US-0068179
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/*tag= b
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/note= "C50S mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "C53S mutation"
                                                                                                                                                                                                                                                                                                                                                                            related proteins, useful for cells against apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236
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Query Match Best Local

Similarity

DB 20; I 1.7e-05;

Length 754;

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RESULT 28
AAH25847
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ABN40537
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UXS
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                     Human apoptosis associated protein 12 and encoded polynucleotide, applicable in diagnosis and treatment of malignant tumour, hemopathy, HIV infection, immunological diseases and various inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; apoptosis associated protein 12; SAG protein 12; cancer; haemopathy; HIV infection; immunological disease; inflammation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human apoptosis associated protein 12 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH25847;
                                                                                                                                                                                                                                                                                  The present invention provides the protein and coding sequences of human apoptosis associated (SAG) protein 12. These sequences can be used in the diagnosis and treatment of malignant tumours, haemopathy, HIV infection, immunological diseases and various types of inflammation. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-AUG-2001
                                                                                                                                                                                                                                                Sequence 1152 BP; 292 A; 265 C; 309 G; 286 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-335831/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-OCT-2000; 2000WO-CN00406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200132863-A1
         Human spliced transcript detection oligonucleotide SEQ ID NO:13285
                                                                                                                                                                                                                                                                        present sequence is the SAG protein 12
                                                                                                                                                                                                                                                                                                                                                Claim 6; Page 22-23; 27pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SHAN-) SHANGHAI BIO DOOR GENE TECHNOLOGY LTD
                                   15-JUL-2002 (first entry)
                                                                                   ABN40537
                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208
                                                                                                                                                 596
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                                                                                                                                                                       71
                                                                                                                                                                                                 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAAGAGGACTGTGTTGTGGTCTGGGGAGA 236
                                                                                                                                                               CAAGAGGACTGTGTTGTGGTCTGGGGAGA 99
                                                                                   standard; DNA; 60 BP
                                                                                                                                                 CAAGAGGACTGTGTTGTGGTCTGGGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.8%; Score 29; ilarity 100.0%; Pred. No. Conservative 0; Mismatci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                   Conservative
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100.0%; Pr
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                                                                                                                                                                                                             Score 29;
Pred. No.
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                                                                                                                                                                                                                No.
                                                                                                                                                   624
                                                                                                                                                                                                                                                                           coding
                                                                                                                                                                                                                           DB 22;
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                                                                                                                                                                                                                                                                           sequence
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                                                                                                                                                                                                                         Length 1152;
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RESULT 30 ABZ11414

ABZ11414 standard;

cDNA;

439

ВP

TXAXAXE

20-JAN-2003 ABZ11414;

(first entry)

Human polynucleotide

SEQ ID NO

296

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The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The libraries are useful for detecting mRNAs from a complete coligonucleotide libraries are useful for detecting mRNAs from a companie coligonucleotide libraries are useful for detecting mRNAs from a companie coligonucleotide libraries are useful for detecting mRNAs from a companie coligonucleotide coligonucleotide coligonucleotide coligonucleotide coligonucleotide sequences from a particular biological or pathology-specific genes such as those genes condition; to detect transcripts of a sub-transcriptome allowing the condition; to detect developmental specific genes such as those genes condition; to detect developmental specific genes; and to detect RNA condition; to detect developmental specific genes; and to detect RNA condition; to detect ABN27253 to ABN39589 represent suffering from a particular disorder. ABN27253 to ABN39589 represent coligonucleotide sequences from rates, humans and mice, which are used in coligonucleotide sequences from rates, humans and mice, which are used in coligonucleotide sequences from rates, humans and mice.
                                                                                                                          Query Match
Best Local S
Matches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New oligonuclectide libraries comprising oligonuclectides which selectively hybridize to mRNAs transcribed from a transcription a genome, useful for detecting tissue-, pathology-, and
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02-MAY-2001; 2001US-287724P.
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splice variant; transcriptome; oligonucleotide library; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-257383/30
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                                                                                                                                                                                                                                                                                                                                                      the exemplification of the present invention.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID 13285; 47pp; English.
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                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences.
36
                                             14 GCCATCTGCAGGGTCCAGGTGATGG 38
                                                                                                                                 25;
                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                              60 BP; 10 A; 13 C; 25 G; 12 T; 0 other;
ĠĊĊĂTĊTĠĊĂĠGGTCCAGGTGATGG
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100.0%;
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                                                                                                                                                                                                   DB 24;
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RESULT 31
AAC77493
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DE Huma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleotide sequence selected from any of 948 sequences (ABZI1119-ABZI2066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful for identifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight markers, as a food supplement, for generating antibodies, in medical imaging, screening and dispostic assays and for treating cell-proliferative disorders (cancer), neurodegenerative diseases
Human ORFX ORF3048 polynucleotide sequence SEQ ID NO:6095
                                                                                                                                                                                                                                                                                                                                                                      (Parkinson's or Alzheimer's disease), autoimmune diseases (multiple sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid disorders, platelet or coagulation disorders, wound, burns, incision, ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal, parasitic), arthritis, etc.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                     08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parkinson's disease; Alzheimer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; infect arthritis; cytostaatic; immunomodulator; nootropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
                                                                                                      AAC77493 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated polynucleotide (I) comprising nucleotide sequence selected from any of 948 sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 296; 1012pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; genome mapping; gene therapy; food supplement; virus; fungus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell-proliferative disorder; neurodegenerative disease; bacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                      231 GCCATCTGCAGGGTCCAGGTGATGG
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                                                                                                                                                                                                                       14
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T, Wang J,
                                                                                                                                                                                                            GCCATCTGCAGGGTCCAGGTGATGG 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or coagulation disorders
                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                          BP;
                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene;
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Ma Y, Yamazaki V, Chen R,
, Wang D, Drmanac RT;
                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                          A; 142 C;
                                                                                                                                                                                                                                                                                          19.7%;
                                                                                                      441
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Pred. No.
                                                                                                                                                                                                                                                                                                                        162 G; 66
                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                      255
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                                                                                                                                                                                                                                                                                       Length 439;
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Z, Ghosh M;
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antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating preventing conditions associated with an ORFX-associated disorder. The mucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allored damage.
                                                                    Query Match
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Matches 25
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                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                         allergies, aplastic anaemia, burns, wounds, bone and cartilage damage nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CURA-) CURAGEN CORP.
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GCCATCTGCAGGGTCCAGGTGATGG 38
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                                                                        Conservative
                                                                                                                                                                                                           BP;
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Pred. No.
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                                                                                                                                                                                                           G; 90
                                                                                                         DB 21;
0.0023;
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                                                                                                                                                                                                              1 other;
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                                                                                                                                                            possible role for SAG in human carcinogenesis. SAG genes, and mutant SAG genes, can be used to protect cells from apoptosis induced by redox reagents. Antisense SAG genes can be used to inhibit the growth of tumour cells. The SAG genes can also be used for the recombinant production of the SAG proteins. The SAG proteins can be used to scavenge oxygen radicals in organisms and to promote wound healing. Additionally, the SAG genes or their complements can be used to promote or inhibit the growth of plant cells (all claimed). The SAG protein is also an ideal molecular target in the development of drugs against neurodegenerative
                                                                                                                                                                                                                                                                                                                                                       This is the nucleotide sequence of deletion mutant 2 of the novel human sensitive to apoptosis gene SAG (see also AAX87314). The cDNA was obtained by PCR amplification of RNA isolated from DLD-1 colon carcinoma cells (ATCC CCT 221). It contains a 48 bp deletion compared with native SAG, starting at nucleotide 177 of the coding region that codes for a potential haem binding site. The in-frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAG gene; sensitive to apoptosis; human; cancer; tumour; neurodegenerative disease; muscular dystrophy; wound healing; vulnerary; therapy; mutant; colon carcinoma; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX87316;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human sensitive to apoptosis
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                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                deletion eliminates 16 amino acids in the encoded protein (see AAY06494) but retains the zinc finger motif. The mutation was detected by PCR in SAG RNA, but not in genomic DNA. It sugges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 15; Page 55-56; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                promoting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-SEP-1998;
19-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (WARN ) WARNER LAMBERT CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sensitive to Apoptosis Gene and related proteins, useful oting cell growth and protecting cells against apoptosis
   151
                             14
                                                          Similarity
25; Conserv
                    GCCATCTGCAGGGTCCAGGTGATGG
   GCCATCTGCAGGGTCCAGGTGATGG 175
                                                                                                                     706 BP;
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97US-0068179.
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                                                                                                                                                   and muscle dystrophy.
                                                                                                                    A; 147
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                                                        Score 25; DB; Pred. No. 0.0 0; Mismatches
                                                                                                                    C; 189 G; 181 T;
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                                                                        DB 20;
0.0023;
                                                                                                                     0 other;
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                                                                                      Length 706;
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RESULT 33
AAL16209
RESULT 34
AAL25052
ID AAL25
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DT 07-DE
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KW Humar
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Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                           The invention relates to human breast cancer expressed polynucleotides (AALO/544-AAL26798) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JAN-2000;
14-MAR-2000;
24-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAL16209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAL16209 standard; cDNA; 264
                                                           07-DEC-2001
                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 1568; 3695pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptide useful as a marker for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-451856/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lillie J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-MAR-2000;
15-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human breast cancer expressed polynucleotide 8666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-DEC-2001
             Human; breast cancer; cell marker; cytostatic; ss
                                 Human breast cancer expressed polynucleotide 17509
                                                                                  AAL25052;
                                                                                                         AAL25052
                                                                                                                                                                                                                                                                                     polypeptides activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JUL-2000;
                                                                                                                                                                                          107
                                                                                                                                                                   57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       breast
                                                                                                                                                                                                                                                               264
                                                                                                         standard; cDNA; 596 BP
                                                                                                                                                                                        CATTCCTTCCACAACTGCTGC 127
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2000US-0205230.
2000US-0211315.
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                                                                                                                                                                                                                                                               BP; 64 A; 59 C;
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2000US-0192099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0220534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0176077
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                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer; cell marker; cytostatic; ss
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                                                                                                                                                                                                                           16.5%;
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                                                                                                                                                                                                                             Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВP
                                                                                                                                                                                                                                                               74 G; 62 T; 5 other;
                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis of breast cancer
                                                                                                                                                                                                                             0.3;
                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                  ٥,
                                                                                                                                                                                                                                        Length 264;
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Homo

sapiens

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RESULT 35
AAL22239
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Best Local Similarity
Matches 21; Conserv
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14-MAR-2000; 2000US-0189167.

24-MAR-2000; 2000US-0192099.

29-MAR-2000; 2000US-0193480.

15-MAY-2000; 2000US-0205330.

09-JUN-2000; 2000US-0211315.

25-JUL-2000; 2000US-0220534.
14-JAN-2000;
14-MAR-2000;
24-MAR-2000;
29-MAR-2000;
15-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic sprinter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 596 BP; 166
                                                                                                                                                                                                                                               WO200151628-A2
                                                                                                                                                                                                                                                                                                                                      Human;
                                                                                                                                                                                                                                                                                                                                                                                     Human
                                                                                                                                                                                                                                                                                                                                                                                                                                  07-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAL22239;
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                                                                                                                                                        10-JAN-2001; 2001WO-US00798.
                                                                                                                                                                                                     19-JUL-2001
                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lillie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide useful as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-451856/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107
                                                                                                                                                                                                                                                                                                                                                                                     breast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATTCCTTCCACAACTGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; cDNA; 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATTCCTTCCACAACTGCTGC
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                2000US-0176077.
2000US-0189167.
2000US-0192099.
2000US-0193480.
2000US-0205230.
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llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                   cancer expressed polynucleotide 14696
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                                                                                                                                                                                                                                                                                                                                           cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
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                                                                                                                                                                                                                                                                                                                                        cell marker;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                        cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        596;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
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RESULT 36
ABQ90662
ID ABQ90
AC ABQ90
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AC ABQ90
XX Micro
XX Micro
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Best Local S
Matches 21
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Lillehaug
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                                                                                            Methylococcus capsulatus genes, oligonucleotides representative
                                      Claim 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M. capsulatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2002
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                                                                            capsulatus
                                                                                                                                    Novel
                                                                                                                                                                          WPI; 2002-557818/59.
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                                                                                                                                                                                                                                                                                                                                                12-JAN-2001;
12-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide useful as a marker
                                                                                                                                  DNA array useful for determining differential expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            array;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                              IJĸ,
                                      Page 318; 678pp; English.
                                                                          genes
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                                                                                                                                                                                                                                                                                                                                                2001NO-0000235.
2001NO-0000239.
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Lossius I,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ds; differential expression;
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                                                                                                                                                                                                                              , Jonassen
Eisen JA,
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                                                                                                                  comprises
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Durkin AS;
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RESULT 37
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Matches 19
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04-FEB-2000
24-FEB-2000
02-MAR-2000
16-MAR-2000
17-MAR-2000
19-MAY-2000
19-MAY-2000
07-JUN-2000
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30-JUN-2000
 07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              number of Methylococcus capsulatus genes. The method of the invention is useful for determination of the differential expression of the genes of M. capsulatus, and for studying gene expression on a genomic scale and in gene expression assays of M. capsulatus genes. The sequences shown in ABQ90016-ABQ91855 represent M. capsulatus genes for use in arrays of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            musculoskeletal system;
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 2000US-0179065

2000US-0184664

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2000US-0199076

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21-SEP-2000

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27-SEP-2000

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02-OCT-2000

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21-SEP-2000;
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2000US-0241787.

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Query Match
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                                                                                                                                                               The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, cother cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune cother cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune cother cancers e.g. Addison's disease, altergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, comultiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) caractiovascular disorders such as myocardial ischaemias; (d) wound chaling; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and of the chious diseases such as viral, bacterial, fungal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.NOV-2000
01-DEC-2000
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                                                                              Sequence
                                                                                         parasitic infections.

Note: The sequence data for this patent did not form part of printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; SEQ ID NO 3347; 781pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.
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17-NOV-2000;
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              ilarity 100.0%; I Conservative 0;
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tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                   14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA encoding novel human musculoskeletal system antigen
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2000US-229509P.
2000US-229513P.
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2000US-234273P.
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2000US-23494P.
2000US-235934P.
2000US-2358347P.
2000US-236327P.
2000US-236367P.
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2000US-226868P.
2000US-228924P.
2000US-229343P.
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2000US-229345P.
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2000US-224519P.
2000US-225267P.
2000US-225268P.
2000US-225270P.
2000US-225447P.
2000US-225757P.
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2000US-217496P.
2000US-218290P.
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2000US-220964P.
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2000US-236368P. 2000US-236369P.

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02-OCT-2000;
13-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
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29-SEP-2000;
29-SEP-2000;
02-OCT-2000;
02-OCT-2000;
                                                                                                                        embryos; increases or decreases the differentiation or proliferation of embryonic stem cells, besides, haematopoietic lineage, modulates mammalian characteristics, such as, body height, weight, hair colour, eye colour, skin, percentage of adipose tissue, pigmentation, size, and shape (e.g., cosmetic surgery); modulates mammalian metabolism; changes mammal's metal state or physical state by influencing biorhythms, caricadic rhythms, depression, tendency for violence, tolerance for pain, reproductive capabilities, hormonal or endocrine levels, appetite, libido, memory, or stress; increases or decreases storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components. This sequence encodes a novel human
                                                                                                                                                                                                                                                                                                                             transports or bone grafts; prevents skin aging due to sunburn by stimulating keratinocyte growth; prevents hair loss, since Fg family members activate hair forming cells and promotes melanocyte growth; stimulates growth and differentiation of hematopoietic cells and bone marrow cells when used in combination with other cytokines; maintains organs before transplantation or for supporting cell culture of primary tissues; induces tissue of mesodermal origin to differentiate in early
                                                                                                                                                                                                                                                                                                                                                                                                                                                        and limb regeneration; stimulates neuronal growth; can treat and prevenerative neuronal damage occurring in certain disorders or neurodegenerative conditions, such as, Alzheimer's disease, Parkinson's disease, and AIDS-related complex; stimulates chondrocyte growth, thus they can be used to enhance bone and periodontal regeneration and aid in tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes an isolated nucleic acid molecule comprising a sequence encoding musculoskeletal system associated polypeptides useful for detecting disorders, e.g., cancer or cancer metastases, in animals or humans. The nucleic acid: stimulates re-vascularisation of ischaemic tissues associated with conditions such as thrombosis, arteriosclerosis,
   Sequence
                                                    printed specification, from the US patent off
                                                                  musculoskeletal system antigen.
Note: The sequence data for this patent did not form printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 3347; 321pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acid molecules associated polypeptides, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosen CA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   other cardiovascular conditions; treats wounds due to injuries,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    post-operative tissue repair, and ulcers; stimulates angiogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROSEN O
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                                                      patent office at
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2000US-241809P.
2000US-244617P.
2000US-249299P.
2000US-251856P.
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2000US-251869P.
                                   .uspto.gov/sequence.html?DocID=20020147140
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2000US-237037P.
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2000US-240960P
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prevent

Best Loca Matches

Local Similarity les 19; Conserv

Conservative (

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Mismatches

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Gaps

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13-FEB-2002

(first entry)

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3.4; DB 25;

Length 498; Indels

15.0%; Score 19; 100.0%; Pred. No.

Query Match

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RESULT 40
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Best Local Similarity
                                                                                                                                                                                                                                                                                      Primer hSAG.M1 corresponds to nucleotides 151-171 of the human sensitive to apoptosis gene (SAG) cDNA clone provided in AAX87314. It was used with primer SAGT.02-1 (see AAX87338) in the RT-PCR amplification of RNA isolated from 20 human tumour lines and transformed lines originating from lung, brain, kidney, prostate, testis, nasopharynx, bone, cervix and foreskin. 2 SAG deletion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX87337 standard; DNA; 18
AAS84630;
                                                                                                                                                                                                                         SAG in human carcinogenesis. SAG (see also AAY06492) is a redox-sensitive, haem-binding protein that promotes cell growth, protects cells from apoptosis, and scavenges oxygen radicals. It
                                                                                                                                                                                                                                                   originating from colon and testis, suggesting a possible role for SAG in human carcinogenesis. SAG (see also AAY06492) is a
                                                                                                                                                                                                                                                                          testis, nasopharynx, bone, cervix and foreskin. 2 SAG mutants (see AAX87315-16) were detected in cancer cell
                                                                                                                                                                                                                                                                                                                                                                                                    SAG: Sensitive to Apoptosis Gene and related proteins, useful promoting cell growth and protecting cells against apoptosis
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                       AAS84630 standard;
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                                                                                                                                                                                                              can be used to reverse a tumour
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19-DEC-1997;
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                                                                                                                                        Conservative
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97US-0068179.
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                       cDNA; 239
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Pred. No. 12;
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RESULT 41
ABX20540/c
ID ABX205
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AC ABX205
AC ABX205
AC ADX205
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DT Human
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                                                                                                                                                                                                                                                                                                                                                                   Delynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sittes expressing (II). (I) and (II) are useful for treating the disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences application of mutations tresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and conditions are coding sequences. AbS44197-AAS94564 represent novel human codi diagnostic coding sequences of the invention.

CC specification, but was obtained in electronic format directly from WIPO and train and not appear in the printed sequence where the invention.
                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 17
Human GDP-mannose 4,6-dehydratase (GM4,6D) DNA #2597
                                   10-FEB-2003
                                                                                                   ABX20540 standard;
                                                                                                                                                                                                                                                                                                                                                          at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptide (II) sequences. (I) is useful as hybridisation proplymerase chain reaction (PCR) primers, oligomers, and for condition of and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of mutat responsible for genetic disorders or other traits and to asse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; ABG20443
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                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                      CCATCTGCAGGGTCCAG 123
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                                                                                                                                                                                                                                                                                                                          239 BP;
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                                (first entry)
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                                                                                                   CDNA; 348
                                                                                                                                                                                                                                                                                                                           A; 87 C;
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100.0%; Pred. No.
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Human breast cell single exon nucleic

acid

probe #5024

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RESULT 42
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03-DEC-1997;
09-SEP-1998;
14-JUN-1999;
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                                                                          01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a composition comprising a human GDP-mannose 4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying GM4,6D inhibitors are useful for reducing inflammation in a mammalian subject and for treating or ameliorating diseases affected
                                                                                                                                                                       ABA46329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               at seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by the level of cellular fucosylation or diseases affected by the fucosylation of glycoconjugates. These diseases include arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 2599; 6pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D) peptide, for manufacturing complex carbohydrates, or as targets for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sullivan F,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 17; Conserv
                                                                                                                                                                                                                                                                                                 205
                                                                                                                                                                                                                                                                                                                                               101
                                                                                                                                                                                                                                                                                                                           TGTAACCATTCCTTCCA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             348 BP; 114 A; 56 C; 75 G; 103
                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                 TGTAACCATTCCTTCCA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GM4,6D antagonists
                                                                                                                                                                                                                                                                                                                                                                                              13.4%;
ilarity 100.0%;
Conservative (
                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kriz R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0149674.
99US-0333177.
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97US-0984246
                                                                                                                                                                     DNA; 355
                                                                                                                                                                                                                                                                                                                                                                                              ٥,
                                                                                                                                                                       ВP
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 17;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for treating e.g. arthritis, or transplant
                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GM4,6D;
                                                                                                                                                                                                                                                                                                                                                                                                                     .
39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                            25; Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene; ss;
                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transplant rejection;
ce; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammation;
                                                                                                                                                                                                                                                                                                                                                                                              <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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RESULT 43
ABA51431
   EXXEXEXEX
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                                                                                                                                                                                                                                                        CC nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting CC the probes with a collection of detectably labelled nucleic acids CC derived from mRNA of human breast, and then measuring the label CC bound to each probe of the microarray. The probes are useful for CC verifying the expression of regions of genomic DNA predicted to CC encode proteins. They are useful for gene discovery, and for CC expression analysis is useful for assessing breast disease. Gene CC expression analysis is useful for assessing the toxicity of chemical CC agents on cells. The microarray of this invention presents a far greater CC diversity of probes for measuring gene expression, with far less bias CC than expressed sequence tag microarrays. The method is suitable for collect the sequence is a single exon nucleic acid probe of the invention. CC Note: The sequence data for this pattent did not form part of the printed specification, but was obtained in electronic format directly crown wide of the intention into published pct sequences.
                                                                                                                                                                                                                      Query Match
Best Local (
                                                                                                                                                                                                             Matches
 Human; microarray; single exon probe; gene expression; breast;
disease; cancer; ss.
                               Human breast cell single exon nucleic acid probe #10126
                                                           01-FEB-2002
                                                                                  ABA51431;
                                                                                                     ABA51431 standard; DNA; 355 BP
                                                                                                                                                                                                                                                      Sequence 355 BP; 122 A; 47 C; 109 G; 77 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-496933/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200157271-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-2001; 2001WO-US00662.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                281
                                                                                                                                                                                     25
                                                                                                                                                                                                         l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprises number of single exon nucleic acid probes
                                                                                                                                                               GGTCCAGGTGATGGATG 297
                                                                                                                                                                                  GGTCCAGGTGATGGATG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 5024; 327pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                                          Conservative
                                                         (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0632366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0608408
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                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                 13.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W,
                                                                                                                                                                                                          0;
                                                                                                                                                                                                                      Score 17;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank DR;
                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                     DB
39;
                                                                                                                                                                                                                                22;
                                                                                                                                                                                                          0,
                                                                                                                                                                                                                               Length 355;
                                                                                                                                                                                                          Indels
                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human
                                                                                                                                                                                                         Gaps
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RESULT 44
ABA56889
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Note: The sequence data for this patent did not form part of the control of the liverity and the part of the control of the liverity of the liverity of the liverity forms of the liverity of the liverity of the liverity forms of the liverity of the liverity forms of the liverity of the liverity forms of the l
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                   01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -
                                                                                                                                ABA56889
                                                                                                                                                                                       ABA56889 standard; DNA; 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; SEQ ID NO 10126; 327pp + sequence listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-496933/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-OCT-2000;
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27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-2000;
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30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200157271-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MOLE-)
                                                                                                                                                                                                                                                                                                                                                  281
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foetal liver single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                               GGTCCAGGTGATGGATG
                                                                                                                                                                                                                                                                                                                                                                                                      GGTCCAGGTGATGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP; 122 A; 47 C; 109 G;
                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.4%;
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   exon nucleic acid probe
                                                                                                                                                                                                                                                                                                                                               297
                                                                                                                                                                                                                                                                                                                                                                                                            41
                                                                                                                                                                                       ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 17;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 355
      #5194.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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Human; foetal Homo sapiens.

liver;

gene

expression; single

exon

nucleic

acid

probe;

SS

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RESULT 45
ABA69454
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Best Local S
Matches 17
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234635.
04-OCT-2000; 2000GB-0024263.
04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.
                                                                                                                                                                                                Human
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 355
                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form printed specification, but was obtained in electronic from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                     01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human
                                                                                       30-JAN-2001;
                                                                                                           09-AUG-2001
                                                                                                                                                     Homo sapiens
                                                                                                                                                                           Human;
                                                                                                                                                                                                                                          ABA69454
                                                                                                                                                                                                                                                               ABA69454 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 5194; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2001
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                                                                                                                                                                                                                                                                                                                     281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genome-derived single exon nucleic acid probes useful zing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                        25
                                                                                                                                                                                               foetal liver single
                                                                                                                                                                        foetal liver; gene expression; single exon nucleic acid probe;
                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                        GGTCCAGGTGATGGATG 41
                                                                                                                                                                                                                                                                                                                    GGTCCAGGTGATGGATG
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                 2000US-0180312.
                                                                                       2001WO-US00669
                                                                                                                                                                                                                     (first
                                                                                                                                                                                                                                                                                                                                                                                                         BP; 122
                                                                                                                                                                                                                                                               DNA; 355
                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                        13.4%;
                                                                                                                                                                                                                                                                                                                                                                                                         A; 47 C; 109 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen
                                                                                                                                                                                                exon
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                                                                                                                                                                                                                                                               ВP
                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                        Score 17;
Pred. No.
                                                                                                                                                                                               nucleic acid probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rank DR;
                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         77
                                                                                                                                                                                                                                                                                                                                                                         39;
                                                                                                                                                                                                                                                                                                                                                                                                        T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  did not form part of
                                                                                                                                                                                                                                                                                                                                                                                  22;
                                                                                                                                                                                                                                                                                                                                                             0,
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                                                                                                                                                                                                                                                                                                                                                              Indels
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RESULT 46
ABA26508
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Best Local S
Matches 17
                                                                                                                        04-FEB-2000; 2000US-0180312.

26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-0234599.

04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                             Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
                                Single
                                                                              Penn
                                                                                                                                                                                                                    30-JAN-2001; 2001WO-US00666
                                                                                                                                                                                                                                           09-AUG-2001.
                                                                                                                                                                                                                                                                 WO200157274-A2
                                                                                                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                ABA26508 standard; DNA; 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                            Probe #4974 for
                                                                                                                                                                                                                                                                                                                                                                                   23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a single exon nucleic acid probe for
                                                                                                    (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity nes 17; Conserv
                                                                             SG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281
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                               exon
                                                                                                    MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 17759; 639pp + sequence listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTCCAGGTGATGGATG
                                                                             Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanzel DK,
                                nucleic
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                                                                                                                                                                                                                                                                                                                                                           gene
                                acid
                                                                                                                                                                                                                                                                                                                                                           expression analysis in human heart
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                                                                             Chen W,
                               probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    %; Score 17; DB
%; Pred. No. 39;
0; Mismatches
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                                                                              Rank
                                for
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                               analyzing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39;
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                               gene
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                                expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                            cell
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                                                                                                                                                                                                                                                                                                                                                           sample.
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                                human
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Claim 1;

SEQ

ID No 4974; 530pp; English

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Best Local S
Matches 17
The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular systematic problems.
                                                                                                                Claim 4; SEQ ID No 14849; 530pp;
                                                                                                                                                          Single exon nucleic acid
                                                                                                                                                                                                                                                                        04-OCT-2000;
                                                                                                                                                                                                                                                                                     21-SEP-2000;
27-SEP-2000;
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03-AUG-2000;
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 congenital heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cardiovascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probe #14849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular systems. Or cardiovascular disease, hypertension, cardiac arrhythmias and prognosity disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The sequence data for this patent did not specification, but was obtained in electronic fo at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                               (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              congeni
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17; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTCCAGGTGATGGATG 41
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                                                                                                                                                                                                                                                                     ;; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0236359.
; 2000US-0224263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression analysis in human heart cell sample
                                                                                                                                                                                                                Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heart; microarray; vascular system; probe; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       355
                                                                                                                                                          probes
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 G;
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                                                                                                                                                       for analyzing gene expression in human
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                                                                                                                English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 355;
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GGTCCAGGTGATGGATG

41

Matches Best Local Query Match

l Similarity 17; Conserv

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Mismatches

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13.4%;
100.0%; A; 47

Score 17; Pred. No.

39;

Length

355;

Sequence

355

BP; 122

C; 109 G;

77

T; 0 other;

brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the

probes which are derived from genomic sequences expressed

invention provides a number of single exon nucleic

in the

human

acid

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RESULT 48
AAK04990
ID AAK04
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Best Local S
Matches 17
                                                                                                                                                                                                       26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e.g. cardiovascular disease, hypertension, congenital heart disease.
Note: The sequence data for this patent did specification, but was obtained in electroni at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                           Single
                                                                                                                            WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                                            Human; brain expressed emicroarray; Alzheimer's
                                                                                   Example 4;
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                                                                                                                                                                                                                                                                                                                     epilepsy;
                                                                                                                                                                                                                                                                                                                                                     Human brain expressed single
                                                                                                                                                                                                                                                                                                                                                                         05-NOV-2001
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                                                                                                                                              SG,
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                                                                                                           exon
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17; Conserv
                                                                                                                                                               MOLECULAR DYNAMICS
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                                                                                                                                                                                                                                                                                                                                                                                                         standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTCCAGGTGATGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      355 BP;
                                                                                                                                             Hanzel DK,
                                                                                                                                                                                                                                                                                                                     cancer;
                                                                                SEQ ID NO: 4981; 650pp + Sequence Listing; English
                                                                                                        nucleic acid probes for analyzing gene expression
                                                                                                                                                                              ; 2000US-0234687.
; 2000US-0236359.
; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                        2000US-0608408.
2000US-0632366.
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                                                                                                                                              Chen W,
                                                                                                                                                                                                                                                                                                                                      exon;
                                                                                                                                                                                                                                                                                                                            disease; multiple
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Pred. No.
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                                                                                                                                              Rank DR;
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                                                                                                                                                                                                                                                                                                                           expression analysis; probe;
multiple sclerosis; schizophrenia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cardiac arrhythmias
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directly from WIPO
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                                                                                                          human
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281

GGTCCAGGTGATGGATG 297

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RESULT 50
AAK30523
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AAK17713
ID AAK17
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Matches 17; Conserv
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-023459.
04-OCT-2000; 2000GB-0024263.
Human bone marrow expressed single exon probe SEQ ID NO: 5080.
                                                                                                                                                                                                                                                                 probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                 AAK30523;
                                                                                                                                                                                                                                  Sequence 355 BP; 122 A; 47 C; 109
                                                                                                                                                                                                                                                                                                                                                                                               Single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-483446/52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                         06-NOV-2001
                                                                        AAK30523 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                   The present
                                                                                                                                                                                                                                                                                                                                                         Example 4; SEQ ID NO: 17704; 650pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001; 2001WO-US00667
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                                                                                                                                                          GGTCCAGGTGATGGATG 41
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                                                                                                                                                                                                                                                                                                                                 invention provides a number of single exon nucleic acid
                                                                                                                                                                                   ilarity 100.0%;
Conservative 0;
                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
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                                                                                                                                                                                               13.4%; Score 17; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen W,
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                                                                        ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                             for analyzing gene expression in human
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                                                                                                                                                                                               39;
                                                                                                                                                                                                         DB 22; Length 355;
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Job time : 131.53 secs

7,

2003, 11:58:13

유정

281

GGTCCAGGTGATGGATG

297

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Query Match
Best Local :
                                                     Matches
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03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                  probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
                                                                                                                              Sequence 355 BP; 122 A; 47 C; 109 G; 77 T; 0 other;
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26-MAY-2000;
                                                                                                                                                                                                                                                                                                       Example 4;
                                                                                                                                                                                                                                                                                                                                        analyzing gene expression
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O LOS III	RESULT 2 US-09-252-991 Sequence 11 Patent No. GENERAL INF APPLICANT: ITTLE OF I FILE REFER CURRENT AP CURRENT AP CURRENT AP CURRENT AP I PRIOR APPL PRIOR FILI ORGANISM: ORGANISM:	Query Matc Best Local Matches Qy 8	RESULT 1 US-09-328-352 Sequence 12 Patent No. GENERAL INF. GENERAL INF. APPLICANT: ITILE OF II FILE REFER. CURRENT FAP. CU		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	C C 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MATC J. Rubenfield et al. TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136
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PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Pseudomonas aeruginosa
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SEQ ID NO 200

; LENGTH: 3494

TYPE: DNA

ORGANISM: Homo sapiens
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, LOCATION: (121)..(3024)

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Matches
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APPLICANT: Pasqualini,
TITLE OF INVENTION: MO
TITLE OF INVENTION: MO
TITLE OF INVENTION: Sa
FILE REFERENCE: P.LJ 3
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Best Local Similarity
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Patent No. 6491894
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CURRENT FILING DATE: 2000-09-11
PRIOR APPLICATION NUMBER: 08/926,914
PRIOR FILING DATE: 1997-09-10
PRIOR APPLICATION NUMBER: 08/710,067
PRIOR FILING DATE: 1996-09-10
NUMBER OF SEQ ID NOS: 226
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APPLICANT: Pasqualini, Renata
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
TITLE OF INVENTION: Same
FILE REFERENCE: P-LJ 3203
CURRENT APPLICATION NUMBER: US/09/139,802
CURRENT FILING DATE: 1998-08-25
EARLIER APPLICATION NUMBER: 08/926,914
EARLIER FILING DATE: 1997-09-10
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US-08-961-527-98
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                                                                                                                                                                                                                                                                   Patent No. 6420526
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                Sequence 239, Application US/09149476
                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local:
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Patent No. 6420135
GENERAL INFORMATION:
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                                                                                                           EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
                                                                                                                                                                                      CURRENT
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CURRENT APPLICAT
                                                                                                                                                                                                                                  APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (301) 309-851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB34
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
                 EARLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION UNMER:
APPLICATION NUMBER:
FILING DATE:
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COMPUTER READABLE FORM:
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TYPE: n
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SOFTWARE: ASCII Text
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STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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R APPLICATION NUMBER: 60/038,621
R FILING DATE: 1997-03-07
RR APPLICATION NUMBER: 60/040,626
RR FILING DATE: 1997-03-07
RR APPLICATION NUMBER: 60/040,334
RR FILING DATE: 1997-03-07
                                                                                                                                                                                                                                                                                                                                                                              1105 GACTGTGTTGTGGTCTG 1089
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                                                                                         APPLICATION NUMBER: 60/040,333
FILING DATE: 1997-03-07
                                                                                                                                                       APPLICATION NUMBER: PCT/US98/04493
FILING DATE: 1998-03-06
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17; Conserv
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0; Mismatches
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EARLIER EARLIER EARLIER EARLIER SARLIER APPLICATION NUMBER: 60, FILING DATE: 1997-04-1 APPLICATION NUMBER: 60/ APPLICATION NUMBER: 60/ FTI.TNG DATE: 1997-05-23 APPLICATION NUMBER: FILING DATE: 1997-04-13 APPLICATION NUMBER: 60/043,312 APPLICATION NUMBER: 60/043,669 APPLICATION NUMBER: 60/047,587 FILING DATE: 1997-05-23 APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 1997-05 FILING DATE: FILING DATE: FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/040,163 APPLICATION NUMBER: 60/048,974 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/043,672 APPLICATION NUMBER: 60/043,674 APPLICATION NUMBER: 60/043,671 FILING DATE: 1997-04-11 APPLICATION NUMBER: APPLICATION NUMBER: 60/043,569 APPLICATION NUMBER: 60/043,314 APPLICATION NUMBER: 60/043,568 APPLICATION NUMBER: APPLICATION NUMBER: 60/047,601 APPLICATION NUMBER: APPLICATION NUMBER: 60/047,582 APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: FILING DATE: 1997-05-23 FILING DATE: 1997-05-23 APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: APPLICATION NUMBER: 60/047,617 FILING DATE: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: 60/047,597 APPLICATION NUMBER: 60/047,600 ILING DATE: 1997-05-23 [LING DATE: 1997-04-1] LING DATE: 1997-04-11 CATION NUMBER: 60/047,632 CATION NUMBER: 1997-04-1 1997-04-1 1997-05-23 1997-05-23 1997-05-23 1997-05-23 1997-05-23 1997-05-23 1997-05-23 1997-04-1 1997-04-1 1997-04-1 1997-04-13 1997-04-11 1997-05-23 1997-05-23 1997-05-23 1997-05-23 1997-05-23 1997-05-23 1997-05-23 1997-05-23 1997-05-1997-03-07 60/043,315 60/043,313 60/043,311 60/043,580 60/047,613 60/047,584 60/047,581 60/047,612 60/047,596 60/047,598 60/047,492 60/047,500 60/047,592 60/047,583 60/047,503 60/047,618 60/047,633 60/047,502 60/047,615

FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,893
FILING DATE: 1997-08-22

FILING DATE: 1997-08-22

FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,889 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,877

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RESULT 9
US-09-149-476-76/c
US-09-149-476-76/c
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; Sequence No. 6420526
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CURRENT FILING DATE: 1998-09-08
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TITLE OF INVENTION:
                                                                                                                                                      EARLIER
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                                                                                                                                                                                                                                                                                                         FILE REFERENCE:
                                                                                               EARLIER
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APPLICATION NUMBER: 60/047,615 FILING DATE: 1997-05-23
                                                                  APPLICATION NUMBER: 60/040,336
FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,163
                                                                                                                                                                                                                       APPLICATION NUMBER: 60/040,162 FILING DATE: 1997-03-07
                              FILING DATE:
                                         APPLICATION NUMBER: 60/047,600
                                                        FILING DATE:
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                                                                                                                          APPLICATION NUMBER: 60/040,334
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Pred. No.
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APPLICATION NUMBER: 60/047,589 FILING DATE: 1997-05-23

FILING DATE:

1997-05-23

FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,594 APPLICATION NUMBER: 60/047,590

APPLICATION NUMBER:

60/047,593

FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,578
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,576

FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,614

FILING DATE: APPLICATION I

1997-04-11

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FILING DATE: 1997-01 APPLICATION NUMBER:

LING DATE:

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60/047,586

FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,585

APPLICATION NUMBER: 60/047,588

APPLICATION NUMBER: 60/047,599 FILING DATE: 1997-05-23

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APPLICATION NUMBER: 60/ FILING DATE: 1997-08-22

FILING DATE:

1997-08-22

60/056,845

FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,631

APPLICATION NUMBER: 60/056,864

APPLICATION NUMBER: 60/057,761 APPLICATION NUMBER: 60/056,892 FILING DATE: 1997-08-22

LING DATE: 1997-08-22

APPLICATION NUMBER: 60/047,595

1997-05-23

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APPLICATION NUMBER:

60/056,888

APPLICATION NUMBER: 60/056,903 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,637 APPLICATION NUMBER: 60/056,882 APPLICATION NUMBER: FILING DATE:

LING DATE: 1997-08-22

APPLICATION NUMBER: 60/056,662 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,878 APPLICATION NUMBER: 60/056,630

1997-08-22

60/056,872

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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,894
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,911
FILING DATE: 1997-08-22

APPLICATION NUMBER: 60/056,880

APPLICATION NUMBER: 60/056,879

1997-08-22

LING DATE: 1997-08-22

APPLICATION NUMBER: 60/056,874 FILING DATE: 1997-08-22

APPLICATION NUMBER: 60/056,636 FILING DATE: 1997-08-22

APPLICATION NUMBER: 60/056,910 FILING DATE: 1997-08-22

	NUMBER 1997- NUMBER 1997- NUMBER 1997- NUMBER	NUMBER: 60/043, 1997-04-11 NUMBER: 60/048, 1997-06-06	PPLICATION NUMBER: 60/043,313 ILING DATE: 1997-04-11 PPLICATION NUMBER: 60/043,672 ILING DATE: 1997-04-11	DATE: 1997-04-11	ILING DATE: 1997-04-11 PPLICATION NUMBER: 60/043,669 ILING DATE: 1997-04-11	1997-04-11 NUMBER: 60/043,	1997-04-11 NUMBER: 60/043,	1997-04-11 NUMBER: 60/043,	: 1997-04-11 NUMBER: 60/043,	ILING DATE: 1997-04-11 PPLICATION NUMBER: 60/043,314	PPLICATION NUMBER: 60/043,568	٥, ۵	PPLICATION NUMBER: 60/047,601	TING DATE: 1997-05-23 PPLICATION NUMBER: 60/047,632	PPLICATION NUMBER: 60/047,612) O N	ILING DATE: 1997-05-23 PPLICATION NUMBER: 60/047,582	PPLICATION NUMBER: 60/047,613	00	PPLICATION NUMBER: 60/047,492	0 0	NUMBER: 6	NO.	PPLICATION NUMBER: 60/047,581 ILING DATE: 1997-05-23	PPLICATION NUMBER: 60/047,592 ILING DATE: 1997-05-23	23	23 0/047	ILING DATE: 1997-05-23 PPLICATION NUMBER: 60/047,618	ATION NUMBER: 6	-	ATION NUMBER: 6	PPLICATION NUMBER: 60/047,502 ILING DATE: 1997-05-23
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LING DATE: NUMBER: 60/056,894 1997-08-22

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PLICATION I N NUMBER: 60/0 E: 1997-05-23 NUMBER: NUMBER: 1997-05-23 60/047,589 60/047,594 60/047,590

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ILING DATE: 1997-05-23
PPLICATION NUMBER: 60/047,614
ILING DATE: 1997-04-11
ILING DATE: 1997-05-23
PPLICATION NUMBER: 60/047,501
ILING DATE: 1997-04-11
ILING DATE: 1997-04-11
PPLICATION NUMBER: 60/056,632
ILING DATE: 1997-08-22
PPLICATION NUMBER: 60/056,632
ILING DATE: 1997-08-22
PPLICATION NUMBER: 60/056,644
ILING DATE: 1997-08-22
PPLICATION NUMBER: 60/056,664
ILING DATE: 1997-08-22
PPLICATION NUMBER: 60/056,664
ILING DATE: 1997-08-22
PPLICATION NUMBER: 60/056,664

APPLICATION NUMBER: 60/056,881 FILING DATE: 1997-08-22

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APPLICATION NUMBER: 60/056,909

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                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09816
FILING DATE: 31-UUL-1995
PRIOR APPLICATION NUMBER: US 08/382,454
EPLICATION NUMBER: US 08/382,454
FILING DATE: 01-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,302
APPLICATION NUMBER: US 08/283,302
APPLICATION NUMBER: US 08/283,302
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                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy of COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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les `16; Conser
                                                                                                                                                                                                     FILING DATE:
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APPLICATION NUMBER: 60/056,884
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APPLICATION NUMBER: 60/056,908
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100.0%; Pred. No. 20
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Best Local Similarity
Matches 16; Conserva
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INFORMATION FOR SEQ ID NO:
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                                                                  TELEFAX: (708) 267-53
INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO-Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                              NAME: Pearson, Louise S. REGISTRATION NUMBER: 32,369
REFERENCE/DOCKET NUMBER: ST.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 267-5300
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PRIOR APPLICATION DATA:
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                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                    FILING DATE: 29-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,302
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STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 0 FILING DATE: 01-FEB-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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LOCATION: 6...
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ENGTH:
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nucleic acid
NDEDNESS: unknown
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1717 Deerfield Road
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08/596,387
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; Pred. No.
                                                                                                                                                                                                        STR-4665-CIP2
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PCT-US95-09816A-123
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; LOCATION: 6...
US-09-067-615-123
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Query Match
Best Local Similarity
                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: STR-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 267-5300
TELEFAX: (708) 267-5376
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 123, Application PC/TUS9509816A GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
US 08/382,454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 01 FILING DATE: 01-FEB-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Edwards, Ana C.
APPLICANT: Chavaillaz, Pierre-Andre
APPLICANT: Jiao, Jin-An
TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF
NUMBER OF SEQUENCES: 123
                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                FILING DATE: 29-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                             NAME/KEY: CDS
LOCATION: 6..
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les 16; Conserv
                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: unkn
                                                                                                                                                                                                                                                                                    NAME: Pearson, Louise REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                             TOPOLOGY:
                                                                                                                                                                          ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1243 ACCATTCCTTCCACAA 1258
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                                                                                                                                                                       1382 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grammer, Susan
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                                                             6..1382
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                                                                                                                             unknown
                                                                                                           DNA (genomic)
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                                                                                                                                           unknown
12.6%;
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Score 16;
Pred. No.
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DB 5;
20;
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              Length 1382;
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US-08-596-387B-121
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                                                                    Query Match
Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 01-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
                                                                                                                                                                                                                                               TELEFAX: (708) 267-5376 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09816
FILING DATE: 31-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: ST
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                         WOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release "."
                                                                                                                                                                                                                                                                                                                                     NAME: Pearson, Loui
REGISTRATION NUMBER:
                                                                                                                                           NAME/KEY: CDS
                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
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STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 60015
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                                                                                                                                                                                        FOPOLOGY:
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                                                                                                                                LOCATION:
                                                                                                                                                                                                                                  ENGTH:
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1243
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                             105 ACCATTCCTTCCACAA 120
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                                                                      Similarity
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                                                                                                                                                                                                                 nucleic acid
ACCATTCCTTCCACAA 1258
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                                                                                                                                                                                                                                1385 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1717
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Jiao, Jin-An
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                                                          Conservative
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                                                                                                                             6..1382
                                                                                                                                                                                        unknown
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17 Deerfield Road
                                                                                                                                                                                                                                                                                            (708) 267-5300
                                                                                                                                                                                                                                                                                                                                                                                 29-JUL-1994
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                                                                                                                                                                                                      unknown
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                                                                    12.6%; Score 16; 100.0%; Pred. No.
                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                               US 08/283,302
                                                                                                                                                                                                                                                                                                                                                                                                                                          US 08/382,454
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                                                                                                                                                                                                                                                                                                                                     32,369
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                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Version
                                                                                    DB 2;
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                                                                                    Length 1385;
                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                       0;
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                                                       Gaps
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RESULT 14 US-09-067-615-121

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Sequence 121, Application US/09067615

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                                                                                  Sequence 121, Application PC/TUS9509816A GENERAL INFORMATION:
APPLICANT: Wong, Hing C.
                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (708) 267-5376
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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                                   APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Pearson, Louise S. REGISTRATION NUMBER: 32,369
REFERENCE/DOCKET NUMBER: STI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 267-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 01-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Dade International, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rhode, Peter R.
APPLICANT: Jiao, Jin-An
APPLICANT: Burkhardt, Martin
APPLICANT: Wong. Him
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 29-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                               Local Similarity es 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1385 base pairs
                                                                                                                                                                                                              1243 ACCATTCCTTCCACAA 1258
                                                                                                                                                                                                                                             105 ACCATTCCTTCCACAA 120
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Grammer, Susan
Edwards, Ana C.
Chavaillaz, Pierre-Andre
                                                                                                                                                                                                                                                                             12.6%; Score 16; DB 4; ilarity 100.0%; Pred. No. 20; Conservative 0; Mismatches
                                                    Widanz, Jon A.
                                                                    Rhode, Peter R.
                                                                                                                                                                                                                                                                                                                                                                6..1382
                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
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                                                                                                                                                                                                                                                                                                                 Length 1385;
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US-08-596-387B-122
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                                                                                                                                                                                                                                                                    Sequence 122, Application US/08596387B Patent No. 5869270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (708) 267-53' INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                      APPLICANT: Wong, Hing
TITLE OF INVENTION: MHC
NUMBER OF SEQUENCES: 12:
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09816A
FILING DATE: 31-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Pearson, Louise S.
REGISTRATION NUMBER: 32,369
REFERENCE/DOCKET NUMBER: STI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 267-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                            APPLICANT:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/382,454
FILING DATE: 01-FEB-195
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,302
APPLICATION NUMBER: US 08/283,302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF NUMBER OF SEQUENCES: 123
                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                               COUNTRY:
                                                                                 STATE:
                                                                                                CITY: Deerfield
                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
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                                                     60015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
                                                                                 Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1717 Deerfield Road
                                                                                                               E: Dade International,
1717 Deerfield Road
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Jiao, Jin-An
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                             Peter R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (genomic)
                                                                                                                                                                                MHC COMPLEXES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.6%; Score 16; 100.0%; Pred. No.
                                                                                                                                                               124
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Best Local
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REFERENCE/DOCKET NUMBER: STR-
TELECOMMUNICATION INFORMATION:
TELEPAX: (708) 267-5300
TELEPAX: (708) 267-5376
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 6232445
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 24,
                                            OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                       APPLICANT:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 08/283,302
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APPLICATION NUMBER: PCT/US95/09816
FILING DATE: 31-JUL-1995
                                                                                                                                                                                                                                                                        TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                        APPLICANT:
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APPLICATION NUMBER: FILING DATE: 29-OCT CLASSIFICATION: 536
                                                                              COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                          CITY: Boston
                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: 6...
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                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                           ADDRESSEE:
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16; Conservative
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6232445
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                                                                                                                                                                                                           130 Water Street
                                                                                                                                                                                                                                                                                                        Jiao, Jin-an
Wong, Hing C.
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                                                                                                                                                                                                                        Dike, Bronstein, Roberts & Cushman,
                                                                                                               Diskette
                29-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                     Peter R.
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                               US/08/960,190A
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RESULT 18
US-09-067-615-122
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 122, Appl
Patent No. 6309645
                                                                                                   FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/382,454
FILING DATE: 01-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/283,302
FILING DATE: 29-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/067,615
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                      CLASSIFICATION: PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Pearson, Louise S. REGISTRATION NUMBER: 32,369
REFERENCE/DOCKET NUMBER: STITELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 267-5300
                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wong, Hing
TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF
NUMBER OF SEQUENCES: 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                            FILING DATE
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Corless, Peter REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Deerfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1508 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Dade International, Inc.
1717 Deerfield Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09067615
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Jiao, Jin-An
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                                                                                                                                                                                                                        08/596,387
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                                   STR-4665-CIP2
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RESULT 19
PCT-US95-09816A-122
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; LOCATION: 6...1
US-09-067-615-122
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APPLICATION NUMBER: US 08/382,454
FILING DATE: 01-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,302
FILING DATE: 29-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                    TELBEAX: (708) 267-5376
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 1508 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (708) 267-5376
INFORMATION FOR SEQ ID NO: 122:
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATEN: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09816A
FILING DATE: 31-UUL-1995
CLASSIFICATION:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Edwards, Ana C.
APPLICANT: Chavaillaz, Pierre-Andre
APPLICANT: Jiao, Jin-An
TITLE OF INVENTION: MHC COMPLEXES AND USES THEREOF
NUMBER OF SEQUENCES: 123
                                                                                                                                                                    NAME: Pearson, Louise S.
REGISTRATION NUMBER: 32,369
REFERENCE/DOCKET NUMBER: STI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 267-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1508 base pair
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                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                     TOPOLOGY: un
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Deerfield
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 12.6%; Score 16; DB 4; Local Similarity 100.0%; Pred. No. 20;
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                                                                                   nucleic acid
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1717 Deerfield Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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Edwards, Ana C.
Chavaillaz, Pierre-Andre
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                                                   unknown
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                                DNA (genomic)
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                                                                    unknown
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, LENGTH: 3208
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-780-016-27
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US-09-780-016-27
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PCT-US95-09816A-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-194-285-7
                                                                                                                                                                                                                                                                                                           APPLICANT: Webb, Susan R.
APPLICANT: Wingvist, Ola
APPLICANT: Karlsson, Lars
APPLICANT: Jackson, Michae
APPLICANT: Peterson, Per I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 12.6
Best Local Similarity 100.
Matches 16; Conservative
                                                                SOFTWARE:
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                                                                                                  CURRENT APPLICATION NUMBER: US/09/194,285
CURRENT FILLING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: PCT/US97/08697
PRIOR FILING DATE: 1997-05-22
PRIOR APPLICATION NUMBER: US 60/018,175
PRIOR FILING DATE: 1996-05-23
NUMBER OF SEQ ID NOS: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,294
PRIOR FILING DATE: 2000-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Donoho, Gregory
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Jenn
                                                                                                                                                                                                                                                 APPLICANT: Peterson, Per A.

TITLE OF INVENTION: MHC Class II Antigen Presenting Systems
TITLE OF INVENTION: and Methods for Activating CD4+ T Cells
FILE REFERENCE: TSRI 536.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: No. 6509456el Human Proteases TITLE OF INVENTION: Polynucleotides Encoding the FILE REFERENCE: LEX-0132-USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 4713
TYPE: DNA
ORGANISM: Mus musculus
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                                                                                   FastSEQ for Windows Version 4.0
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Karlsson, Lars
Jackson, Michael R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zambrowicz, Brian
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20;
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US-08-652-971-1
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                                                                                      RESULT 23
                                                                         US-08-991-258A-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Apprice Patent No. 5814507
                                         Sequence 1, Application Patent No. 5928887
                                                                                                                                                                                                    Query Match
Best Local Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 225-3216
TELEFAX: (415) 952-9881
TELEX: 910 371-7168
INFORMATION FOR SEQ ID NO: 1:
                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 5769 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 225-3216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE, PTP LAMBDA
                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                               890 TTGTGGTCTGGGGAGA 875
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                                                        Application US/08991258A
                                                                                                                                                  TTGTGGTCTGGGGAGA 99
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460 Point San Bruno Blvd.
Cheng,
Lasky,
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             United States
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                                                                                                                                                                                                                                                                                                         DNA (genomic)
 Laurence A.
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100.0%; Pred. No.
tive 0; Mismatc
                                                                                                                                                                                                    100.0%;
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100.0%; Pred. No.
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21;
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RESULT 24
US-08-769-399-1/c
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                                                                                                                                                                                                                                                             sequence 1, Application US/08769399
Patent No. 5976852
GENERAL INFORMATION:
APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY:
LOCATION:
                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: A-TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER: DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                   APPLICANT: Lasky, Laurence A. TITLE OF INVENTION: A NOVEL K TITLE OF INVENTION: PHOSPHATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 5769 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0
FILING DATE: 17-DEC-1997
CLASSIFICATION: 435
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                      ZIP: 94080
                                                                                                          COUNTRY:
                                                                                                                                          STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 16; Conserv
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                                                                                                                         California
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                                                                                                         United States
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                                                    Floppy disk
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                                                                                                                                                                                                                           PHOSPHATASE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.6%; Score 16;
100.0%; Pred. No.
tive 0; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US 08/652,971
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                                                                                                                                                                                                                                                     KAPPA/MU-LIKE PROTEIN TYROSINE
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                                                                                                                                                                                                                                    PTP LAMBDA
 Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: FILING DATE:

US/08/769,399

CLASSIFICATION:

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RESULT 25
US-08-991-953A-1/c
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Best Local S
Matches 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 910 371-7168
INFORMATION FOR SEQ ID NO: 1:
                                                                            NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-63478-3/WHD/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,971
FILING DATE: 24-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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TELEPHONE: (415) 225-3216
TELEFAX: (415) 952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                 TELEFAX:
                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 16-DEC
                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Dreger, Ginger R. REGISTRATION NUMBER: 33 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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5769 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lasky, Laurence A.

IVENTION: A NOVEL KAPPA/MU-LIKE PROTEIN TYROSINE

IVENTION: PHOSPHATASE, PTP LAMBDA
                                                                 (415)
                                                                                                                                                                                                                                                                                                                                                                                                     United States
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.6%; Score 16; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
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379..4686
                                                                                                                                                                                                                                                                                                                   E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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16-DEC-1997
N: ^эг
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21;
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Best Local Similarity
Thes 16; Conserv
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Query Match 11.8%; So Best Local Similarity 100.0%; I Matches 15; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 60434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 196 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: WO PCT/JP94/02288
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 93/352858
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/663,082
                                                                                                         ORIGINAL SOURCE
                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 81
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2
CLASSIFICATION:
                                                                          STRAIN:
                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                          NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                         ORGANISM:
                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington
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                                                                          IAM M-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                               (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NISHIZAWA, Osamu
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379..4686
                                                                                         Anabaena variabilis
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                                                                                                                                     double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENE FOR FATTY ACID DESATURASE, VECTOR
                                                                                                                                                                                                                                                                                          29,768
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Score 15; DB 3; Pred. No. 67; 0; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                             81356/107
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                            Length 196;
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 Indels
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Gaps
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RESULT 29
US-09-702-705-1559
; Sequence 1559, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
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NAME/KEY: misc_feature

OTHER INFORMATION: Incyte ID No. 6476212 700612036H1

NAME/KEY: unsure

LOCATION: 128

OTHER INFORMATION: a, t, c, g, or other

US-09-313-294A-3641
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US-09-328-352-2677
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APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOUTWARE: PERL PROGram
SEQ ID NO 3641
LENGTH: 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: GRIY L. Breton et al.
APPLICANT: GRIY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUWANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT PELICATION NUMBER: US/09/328,352
CURRENT PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 2677
LENGTH: 219
                                                                                                                                                                                                 Matches
                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3641, Application US/09313294A Patent No. 6476212
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Best Local Similarity
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Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Zea mays
                                                                                                                            154 GATGTCAAGCTGAAA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 CTGAAAACAAGCAAG 115
                                                                                                                                                          51 GATGTCAAGCTGAAA 65
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100.0%; Pred. No.
tive 0; Mismatc
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                                                                                                                                                                                                               Score 15;
Pred. No.
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                                                                                                                                                                                                                  DB 4;
67;
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67
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APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
FILE REFERENCE: 210121.479C14
CURRENT APPLICATION UNMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1559
LENGTH: 266
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                                                                                                                               ; SOFTWARE: FASTSEQ for V
SEQ ID NO 1559
; LENGTH: 266
; TYPE: DNA
; ORGANISM: Homo sapien
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US-09-736-457-1559
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Best Local Similarity 100.
Matches 15; Conservative
                                                      Query Match
Best Local Similarity
Matches 15; Conserv
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APPLICANT:
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Patent No. 6509448
                                                                                                                                                                                                     APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
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APPLICANT:
APPLICANT:
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196 GCTGAAAACAAGCAA 210
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                          59 GCTGAAAACAAGCAA 73
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                                                                                                                                                                                            FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                Mannion, Jane
Fan, Liqun
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Vedvick, Tom
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Bangur, Chaitanya
Lodes, Michael A.
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Carter, Darrick
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Bangur, Chaitanya
Lodes, Michael A.
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                                                          Conservative
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                                                      11.8%; Score 15;
100.0%; Pred. No.
:ive 0; Mismatc
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                                                          Mismatches
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RESULT 31 US-09-313-294A-2588/c US-09-313-294A-2588, Application US/09313294A ; Patent No. 6476212 ; GENERAL INFORMATION:

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; OTHER INFORMATION: Incyte ID No. 6476212 700552942H1
US-09-313-294A-2588
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CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 2588
LENGTH FOR
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Best Local Similarity
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GENERAL INFORMATION:
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TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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TYPE: DNA
ORGANISM: Zea mays
                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/016,434

FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
                                                                                                                                                                                             NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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               TOPOLOGY: line
IMMEDIATE SOURCE:
LIBRARY: BRSTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                    STRANDEDNESS:
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CALIFORNIA
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Ito, Laura Y.
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961450
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3174 PORTER DRIVE
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                 BRSTTUT03
                                                   linear
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                                                                    single
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67;
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                                                                              US-08-412-614-93
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Best Local Similarity
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Sequence 93, App.--
Sequence 93, App.--
Query Match
Best Local Similarity
Matches 15; Consert
                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 07/965,394
FILING DATE: 17-DEC-1992
APPLICATION UNMBER: PCT/EP91/00743
FILING DATE: 18-APR-1991
PRIOR APPLICATION DATA:
APPLICATION UNMBER: GB/90901054.3
APPLICATION UNMBER: GB/90901054.3
FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hillson, Randall A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                     TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette 3.5 inch, 1.44 mb capacity COMPUTER: IBM PC compatible (Compaq Deskpro 286e) OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect Version #5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/412,614
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TITLE OF INVENTION:
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MEDIUM TYPE: Diskett
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TITLE OF INVENTION: Hybridization Probes Derived from the
TITLE OF INVENTION: Spacer Region Between the 16S and 23S rRNA Genes for the
TITLE OF INVENTION: Detection of No. 5536638-Viral Microorganisms
                                                                                                                               ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 612-332-5300
                                                                                                                                                                 TOPOLOGI. DN
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CITY: Minneapolis
                                                                                              ORGANISM: Haemophilus influenzae STRAIN: NCTC 8143
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REFERENCE/DOCKET NUMBER:
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3100 No. 5536638west Center
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                             11.8%; Score 15; DB 1; 100.0%; Pred. No. 68;
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                                                                                                                                                                                                                                                                                                                                                                           31,838
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                Mismatches
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67;
                0;
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                                                 Length 474;
                  Indels
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                   Gaps
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56 CAAGCTGAAAACAAG 70

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CAAGCTGAAAACAAG 272

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; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-635-761-93
                                                                                                                                                               RESULT 35
US-09-312-520-93
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US-08-635-761-93
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Best Local (
                                                                                                                            Sequence 93, Application US/09312520 Patent No. 6277577
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Sequence 93, App...
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PRIOR APPLICATION: 435
APPLICATION NUMBER: 07/965,394
FILING DATE: 17-DEC-1992
APPLICATION NUMBER: 08/412,614
FILING DATE: 29-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hillson, Randall A
REGISTRATION NUMBER: 31,838
REFERENCE/DOCKET NUMBER: 8076.75USC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/332-5300
                               GENERAL INFORMATION:
APPLICANT: ROSSAU, RUDI
TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER REGION
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
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APPLICANT: Rossau,
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 474 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 19-APR-1996
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CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
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                      ADDRESSEE:
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                                                                                                                                                                                                                                    258 CAAGCTGAAAACAAG 272
                                                                                                                                                                                                                                                                      56 CAAGCTGAAAACAAG 70
                                                                                                                                                                                                                                                                                                                            Similarity
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E: Merchant, Gould, Smith, Edell, Welter & Schmidt 3100 No. 6277577west Center, 90 S. 7th Street
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VENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER REGION BE
                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                     11.8%; Score 15;
100.0%; Pred. No.
/ative 0; Mismatc
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US-08-412-614-94
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Patent No. 5536638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: Ger HYPOTHETICAL: NO ANTI-SENSE: NO
                                         ZIP: 55402-4131

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 inch,
COMPUTER: IBM PC compatible (Cor
OPERATING SYSTEM: MS-DOS
COPETANDE: MONTH MS-DOS
                                                                                                                                                                                                                                             APPLICANT: Rossau, Rudi
APPLICANT: Van Heuverswyn, Hugo
TITLE OF INVENTION: Hybridization Probes Derived from the
TITLE OF INVENTION: Spacer Region Between the 16S and 23S rRNA Genes for the
TITLE OF INVENTION: Detection of No. 5536638-Viral Microorganisms
               SOFTWARE: Wordperfect Version #5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 31,838
REFERENCE/DOCKET NUMBER: 8076.75USC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 29-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hillson, Randall A
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PRIOR APPLICATION DATA:
07/965,394
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                                                                                                                                                                   STREET:
                                                                                                                                                 STATE:
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FILING DATE: 17-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0 FILING DATE: 19-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 612/332/9081
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                                                                                                                                                               Minneapolis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d: 474 base pairs
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3100 No. 5536638west Center
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100.0%; Pr
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US/08/412,614
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FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER:

07/965,394

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 5945282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 17-DEC-1992
APPLICATION NUMBER: PCT/EP91/00743
FILING DATE: 18-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB/90901054.3
FILING DATE: 18-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hillson, Randall A.
                                             APPLICATION NUMBER: US/08/635,761
FILING DATE: 19-APR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/965,394
FILING DATE: 17-DEC-1992
APPLICATION NUMBER: 08/412,614
FILING DATE: 29-MAR-1995
ATTORNEY/AGENT INFORMATION:
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HYPOTHETICAL: N
ANTI-SENSE: NO
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ORGANISM: Haemo:
STRAIN: ITM 859
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ROSSAU, RUDI
TITLE OF INVENTION: HYBRIDIZATION PROBES DERIVED FROM THE SPACER REGION BE
                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                      COMPUTER: IBM COOPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                     STREET: 3100
CTTY: Minneapolis
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                                                                                                                                                                                                                             SOFTWARE: FastSEQ Version 1.5
REFERENCE/DOCKET NUMBER: 80
                                NAME: Hillson, Randall A
                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 5945282west Center, 90 S. 7th Street
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STRANDEDNESS: single
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   8076.75USC1
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RESULT 38
US-09-312-520-94
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/96
FILING DATE: 17-DEC-1992
APPLICATION NUMBER: 08/41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: G
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 base pairs
TYPE: nucleic acid
HYPOTHETICAL: NANTI-SENSE: NO FRAGMENT TYPE:
                                                                                                                                                                                              NAME: Hilson, Randall A
REGISTRATION NUMBER: 31,838
REFERENCE/DOCKET NUMBER: 8076.75USC1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 476 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/312,
FILING DATE: 19-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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NUMBER OF SEQUENCES:
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                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                  FILING DATE: 29-MAR-1995
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM:
                                                                  STRANDEDNESS
TOPOLOGY: 1:
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STREET: 3100 No. 6277577west Center, 90 S. 7th Street
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                                                                                                                                                                                                                                                                                                                       08/412,614
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US-09-121-425-3

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US-08-309-182B-2
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                                                     Matches
                                                                             Query Match
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                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 819 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: No. 56396
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: September 20, CLASSIFICATION: 435
PRIOR APPLICATION DATA, APPLICATION NUMBER:
                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                            NAME/KEY: CDS
LOCATION: 1.816
IDENTIFICATION METHOD:
                                                                Local Similarity
                                                                                                                                                                                                                                 TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                  TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: Septem
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                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                            IOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITY: Washington
  521
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                         84
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                                                    15;
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                 TIGTGGTCTGGGGAG 98
TTGTGGTCTGGGGAG
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                                                    Conservative
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                                                                                                                                                                                              Genomic DNA
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                                                                                                                                                                                                                     double
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100.0%; Pr/
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                                                                100.0%;
                                                                            11.8%;
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Street, N.W., #700
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                                                                Score 15; ; Pred. No.
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Pred. No.
                                                    Mismatches
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                                                                DB 1;
68;
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68;
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                                                                         Length 819;
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RESULT 40

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RESULT 42
US-08-389-668A-1/c
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Best Local Similarity
Watches 15; Conserva
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US-09-634-493A-3
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Best Local Similarity
Matches 15; Conserve
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LENGTH: 1426
TYPE: DNA
                                            Sequence 1, Application US/08389668A Patent No. 5637470
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Applic Patent No. 6153418
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                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: consensus phytases 13239
CURRENT APPLICATION NUMBER: US/09/634,493A
CURRENT FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: US/09/121,425
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: EPO 97112688.3
PRIOR FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER APPLICATION NUMBER: EPO 97112688.3 EARLIER FILING DATE: 1997-07-24 NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Consensus Phytases
FILE REFERENCE: consensus phytases 13239
CURRENT APPLICATION NUMBER: US/09/121,425
CURRENT FILING DATE: 1998-07-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Consensus Phytases
                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1426
TYPE: DNA
ORGANISM: Artificial Sequence
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                               APPLICANT:
   APPLICANT:
                                                                                                                                                              1250 ATGTCAAGCTGAAAA 1264
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Kaczorowski, Gregory J. Garcia, Maria L. Leonard, Reid J.
                                                                                                                                                                                                                          Conservative 0;
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                                                                                                                                                                                                                                                                                                      Description of Artificial Sequence:consensus sequence
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100.0%; Pred. No.
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RESULT 43
US-08-732-506-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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NFORMATION FOR SEQ ID NO: 1:
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 08/242,811
FILING DATE: 13-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
COMPUTER: IBM FC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                             APPLICANT: Folande TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Francis P. Bigley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                           STREET:
 OPERATING SYSTEM:
                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: do:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Bigley, Francis
REGISTRATION NUMBER:
                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Rahway
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                          INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H: 2238 base pairs nucleic acid ADEDNESS: double
                                                                 07065-0900
                                                                                                            Rahway
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                                                                                             New Jersey
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                                                                                                                           E: Francis P. Bigley
126 E. Lincoln Avenu
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                                                                                                                                                                                   McManus, Owen B.
Swanson, Richard J.
Folander, Kimberly L.
FOLENTION: NOVEL HETEROMULTIMER
                                                                              USA
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                                                                                                                                                                                                                                                                          Garcia, Maria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                         Leonard, Reid
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                                                                                                                                                                                                                                                                                      Kaczorowski, Gregory J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (908) 594-1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA to mRNA
PC-DOS/MS-DOS
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                                                                                                                             Avenue,
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                                                                                                                             P.O.
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69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application PC/TUS9505768 GENERAL INFORMATION:
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Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (908) 594-427 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                            APPLICATION NUMBER: US 00 FILING DATE: 13-MAY-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
TELECOMMUNICATION INFORMATION: TELEPHONE: (908) 594-1249
                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 2238 base pairs
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TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/08/732,506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: cDNA to mRNA
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                              NAME: Bigley, Francis P. REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
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APPLICATION NUMBER:
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EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                            INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGCTGAAAACAAGC
                                                                                                                                                                                                                                                                                                                           New Jersey
                                                                                                                                                                                                                                                                                                                                                        126 E. Lincoln Avenue, P.O. Box 2000
                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                       Folander, Kimberry L.
VENTION: NOVEL HETEROMULTIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Garcia, Maria L.
Leonard, Reid J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McManus, Owen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Swanson, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaczorowski, Gregory J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                           Francis P. Bigley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (806)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   594-4270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   594-1249
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                                                                                                              US 08/242,811
                              36,356
AFR: 19226
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                                                                                                                                                                                PCT/US95/05768
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                                                                                                                                                                                                               Version
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69;
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Query Match
Best Local Similarity
Watches 15; Conserve
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                                                                                                  ; NAME/KEY:
; LOCATION:
US-07-959-943-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/07/959,943
FILING DATE: 19921014
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405.38a
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                     TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                           FEATURE:
                                                                                                                                                                   MOLECULE TYPE: CDN POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Blakely, Randy D. APPLICANT: Fremeau Jr., Robe APPLICANT: Caron, Marc G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Raleigh STATE: No. 5418162th Carolina COUNTRY: U.S.A.
                                                                                                                                                          UNITS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U
ZIP: 27622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                   POPOLOGY:
                                                                                                                                                                                                                                         ENGTH:
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23 AGGGTCCAGGTGATG 37
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                                                                                                                                                                                                                          nucleic acid
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5418162
                                                                                                                                                       2278 basepairs
                                                                                                                                                                                                                                        2508 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B: Gibson Post Office Drawer 31107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.8%; So ilarity 100.0%; E Conservative 0;
                                            Conservative
                                                                                                              CDS
73..1962
                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kenneth D. Sibley; Bell, Seltzer, Park
                                                                                                                                                                                   CDNA
                                                                                                                                                                                                               single
                                                      11.8%; Score 15;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serotonin Transporter cDNA
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Pred. No.
                                            Mismatches
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69;
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69;
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                                                                     Length 2508;
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                                          Indels
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US-09-074-658-69/c
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                                                                                                                                                                                                                         US-09-620-312D-552/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 69, Appl
Patent No. 618437
                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
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GENERAL INFO...

APPLICANT: Tang, Y. 10...

APPLICANT: Liu, Chenghua

APPLICANT: Asundi, Vinod

APPLICANT: Zhang, Jie

APPLICANT: Ren, Feiyan

APPLICANT: Chen, Rui-hong

APPLICANT: Zhao, Qing A.

""h'TCANT: Thao, Qing A.
                                                                                                                                                                                                                                            Sequence 552, Application US/09620312D Patent No. 6569662
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Stewart, Michael I
REGISTON NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPA
OPERATING SYSTEM: PC-D
SOFTWARE: PATENTIN Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Quijun Wang
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 08-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 6th F1 CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                          442 TACCTGTGCCATCTG 428
                                                                                                                                                                                                                                                                                                                                                                                     7 TACCTGTGCCATCTG 21
Wehrman, Tom
Xue, Aidong J.
Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09074658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2718 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (416) 595-1163
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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100.0%; Pred. No.
tive 0; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3;
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В
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, NAME/KEY: misc_feature

; LOCATION: (1)...(3582)

; OTHER INFORMATION: n = a,t,c or g

US-09-620-312D-552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 552
LENGTH: 3582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/620,312D CURRENT FILING DATE: 2000-07-19 PRIOR APPLICATION NUMBER: 09/552,317. PRIOR FILING DATE: 2000-04-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6559662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/488,725 PRIOR FILING DATE: 2000-01-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                              FILING DATE: 30-JUN-1992
APPLICATION NUMBER: JP 215017/1992
FILING DATE: 12-AUG-1992
APPLICATION NUMBER: JP 303878/1992
APPLICATION NUMBER: JP 303878/1992
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: PASSIVE CREATERS
                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MASAYOShi MISHINA
TITLE OF INVENTION: NOVEL PROTEINS AND GENES CODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OCATION: (392)..(2647)
                   NAME: Hamburg, C.Bruce
REGISTRATION NUMBER: 2
                                                                                                                                                                  FILING DATE: 26-FE
                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 26-FEB
                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: MS-DOS v.5
SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Niigata-shi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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John Tillinghast
                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Nishiohata Residence 1-107
5214, Nishiohata-machi
                                                                                                                                                                                                                                                                                                                                                                                                              JAPAN
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                                                                                                                                                                                                                                                                                                                                IBM Compatible
                                                                                                                                                              26-FEB-1992
UMBER: JP 173155/1992
                                                                                                                                                                                                                                                                                                                                                  Diskette,
                                                                                                                                                                                                                                            26-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.8%; Score 15;
100.0%; Pred. No.
                                                                                                                                                                                                       JP 39563/1992
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F-4551
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                                                                                                                                                                                                                                                                                                                                                    1.44 MB storage
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RESULT 49
US-08-026-138E-6/c
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                                                                   REGISTRATION NUMBER: 22,389
REFERENCE,DOCKET NUMBER: F-45
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 986-2340
TELEPAX: (212) 985-7733
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-026-138E-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/026,138E FILING DATE: 26-FEB-1993
PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION UMBER: JP 39563/1992
FILING DATE: 26-FEB-1992
APPLICATION NUMBER: JP 173155/1992
FILING DATE: 30-JUN-1992
APPLICATION NUMBER: JP 215017/1992
FILING DATE: 12-AUG-1992
APPLICATION NUMBER: JP 303878/1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212) 953-7733
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: cDN/
ORIGINAL SOURCE:
ORGANISM: mouse
TISSUE TYPE: brai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Word Perfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Masayosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 986-2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Com
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS: Masayoshi MISHINA
TITLE: NOVEL PROTEINS AND GENES CODING THE SAME
RELEVANT RESIDUES IN SEQ ID NO: 17: FROM 1 to 4368
                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Niigata-shi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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                                                      ENGTH:
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                             nucleic acid
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                                                      4446 nucleic acids
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5214, Nishiohata-machi
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GENERAL INFORMATION:
APPLICANT: Wisconsin Alumni Research Foundation
APPLICANT: Hutchinson, Charles R.
APPLICANT: Kennedy, Jonathan n.m.i
APPLICANT: Kennedy, Jonathan n.m.i
APPLICANT: Park, Cheonseok n.m.i
TITLE OF INVENTION: METHOD OF PRODUCING ANTHYPERCHOLESTEROLEMIC AGENTS
FILE REFERENCE: 960296.95718
CURRENT APPLICATION NUMBER: US/09/215,694B
CURRENT APPLICATION NUMBER: US/09/215,694B
CURRENT FILING DATE: 1999-12-18
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 5053
TYPE: DNA
GRGANISM: Aspergillus terreus
US-09-215-694-20
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Search completed: November 7, 2003, 11:59:33 Job time: 37.4064 secs
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US-09-215-694-20/c
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                                                                                                                                                                                          Query Match 11.8%; Score 15; DB 4; Length 5053; Best Local Similarity 100.0%; Pred. No. 70; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 11.8%; Score 15; DB Best Local Similarity 100.0%; Pred. No. 70 Matches 15; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: mouse
ORIGINAL SOURCE:
ORGANISM: mouse
TISSUE TYPE: brain
PUBLICATION INFORMATION:
AUTHORS: Masayoshi MISHINA
TITLE: NOVEL PROTEINS AND GENES CODING THE SAME
RELEVANT RESIDUES IN SEQ ID NO: 6: FROM 1 to 4446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3359 TTGTGGTCTGGGGAG 3345
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210 CCAGGTGATGGATGC 196
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Result
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Maximum DB
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Perfect score:
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s derived by a
       Published_Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US05_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US05_PUBCOMB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

15: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US00B_PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US00B_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US00B_PUBCOMB.seq:*
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length: 2000000000
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               US-10-108-767-7
US-10-152-156-7
US-09-796-692-8547
US-10-040-862-8547
US-10-040-862-8547
US-09-764-864-39
US-09-764-864-39
US-10-198-846-12407
US-09-908-975-13285
US-10-198-846-7306
US-10-198-846-7306
US-09-764-877-3347
US-09-764-877-3347
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827.407 Million cell updates/sec
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               Sequence 7, Appli
Sequence 7, Appli
Sequence 8547, Ap
Sequence 8547, Ap
Sequence 8547, Ap
Sequence 396, App
Sequence 396, App
Sequence 12407, A
Sequence 13285, Ap
Sequence 13318,
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3686	3686	3686	3681	3494	3494	3494	3494	2904	1781	1781	712	712	575	575	500	481	464	355	355	348	252	252	930	930	833	833	833	833
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-10-084-817-8	US-10-044-090-218	-09-981-353-1	-10-133-013-	US-10-281-904-1	-10-264-374-2	-823-	9-880-107-	-10-281-		US-10-027-632-255720	US-10-027-632-145248	-10-027-632-145	-10-027-632-22479	-10-027-632-	-09-918-995-3185	US-09-878-574-1344		US-09-864-761-21703	1-4	-878-	US-10-027-632-276727	٠	-10-027-632-31	-10-027-632-310	-10-027-632-1629	-10-027-632-1629	-10-027-632-1629	32-1
equence 8	e 218,	equence 121,	e 221,	Sequence 1, Appli	equence 200	e 31,	e 229	e u	e 2	equence 2!	equence 1	Sequence 145248,	e 2	2247	51	1344	e 1656,		4974, 1	equence	e 27672	Sequence 276727,	31061,	310	16298	equence 162	equence 16298	298

ALIGNMENTS

## ; LENGTH: 342 ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-826-312-7 RESULT 1 US-09-826-312-7 APPLICANT: Sheung, Julie APPLICANT: Pray, Todd R. TITLE OF INVENTION: UBIQUITIN LIGASE ASSAY FILE REFERENCE: A-68613-1/RMS/JJD CURRENT APPLICATION NUMBER: US/09/826,312 CURRENT FILING DATE: 2001-04-03 PRIOR APPLICATION NUMBER: US 09/542,497 PRIOR FILING DATE: 2000-04-03 NUMBER OF SEQ ID NOS: 17 Query Match 25.2%; Best Local Similarity 100.0%; Matches 32; Conservative SOFTWARE: PatentIn version 3.1 SEQ ID NO 7 Sequence 7, Application US/09826312 Patent No. US20020042083A1 GENERAL INFORMATION: APPLICANT: Issakani, Sarkiz APPLICANT: Huang, Jianing 151 GCCATCTGCAGGGTCCAGGTGATGGATGCCTG 182 14 GCCATCTGCAGGGTCCAGGTGATGGATGCCTG 45 U Score 32; DB b; Pred. No. 1.7 0; Mismatches 0, DB 9; 1 Length 342; Indels

RESULT 2
US-10-108 767-7
; Sequence 7, Application US/10108767
; Publication No. US20030104474A1
; GENERAL INFORMATION:
; APPLICANT: Issakani, Sarkiz D.
; APPLICANT: Huang, Jianing

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                                                                                                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-152-156-7
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SEQ ID NO 7
                                                                                                                                                                                                              SEQ ID NO 7
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Best Local
                                         Best Local Similarity Matches 32; Conserv
                                                                               Query Match
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CURRENT APPLICATION NUMBER: US/10/108,767
CURRENT FILING DATE: 2002-09-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sheung, Julie
APPLICANT: Pray, Todd R.
APPLICANT: Pray, Todd R.
TITLE OF INVENTION: ASSAYS FOR IDENTIFYING UBIQUITIN AGENTS
TITLE OF INVENTION: MODIFY THE ACTIVITY OF UBIQUITIN AGENTS
FILE REFERENCE: A-68613-6/RMS/DCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 10/091,139
PRIOR FILING DATE: 2002-03-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 09/542,497 PRIOR FILING DATE: 2000-04-03
                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version
                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2002-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 09/826,312
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 10/091,174
PRIOR FILING DATE: 2002-03-04
PRIOR FILING DATE: 2002-03-04
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CURRENT FILING DATE: 2002-05-20
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PRIOR APPLICATION NUMBER: US 10/109,460
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TILE OF INVENTION: ASSAYS FOR IDENTIFYING UBIQUITIN AGENTS AND FOR IDENTIFYING AGENT
TILE OF INVENTION: MODIFY THE ACTIVITY OF UBIQUITIN AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 342
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    GCCATCTGCAGGGTCCAGGTGATGGATGCCTG 45
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                                                                                                                                                                                                                                                                                                 CATION NUMBER: US 60/291,836
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                                         Conservative
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Sequence 8547, Application US/10040862
Publication No. US20030078396A1
GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 9597
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8547
LENGTH: 612
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PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
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CURRENT FILING DATE: 2001-03-01
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APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
APPLICANT: Corporation
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
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PRIOR APPLICATION NUMBER: 60/202,084
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LOCATION: (485)
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32; Conser
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PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545

CURRENT APPLICATION NUMBER: US/10/040,862

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; SOFTWARE: PatentIn Ver. 2; SEQ. ID NO 39; LENGTH: 836; TYPE: DNA; ORGANISM: Homo sapiens US-09-764-864-39
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US-09-764-864-39
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                                   Matches
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Best Local Similarity
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Best Local Similarity
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TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PTZ23
CURRENT APPLICATION NUMBER: US/09/764,864
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COFTWARE: FastSEQ for Windows Version
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APPLICATION NUMBER: US 60/202,084
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14 GCCATCTGCAGGGTCCAGGTGATGGATGCCTG 45
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Pred. No.
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Pred. No.
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RESULT 9

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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 14, 24, 32, 206, 240, 361,
; OTHER INFORMATION: n = A,T,C or G
US-10-102-524-396
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CURRENT FILING DATE: 2002-03-19
NUMBER OF SEQ ID NOS: 1863
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 396
LENGTH: 535
TYPE: DNA
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Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
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SEQ ID NO 498
LENGTH: 836
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Best Local
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CURRENT FILING DATE: 2001-01-17
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF KIDNEY
FILE REFERENCE: 210121.572
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NAME/KEY: SITE
LOCATION: (45)
OTHER INFORMATION: n equals a,t,g, or c
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71
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Gordon, Brian
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o. US20030109434A1
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Pred. No. 1.6e-07;
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Pred. No.
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99
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7.1e-06;
hes 0;
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                                                                                              Length 535;
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US-10-198-846-12407
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                                                                                                                     ; TYPE: DNA; ORGANISM: Homo sapiens US-09-908-975-13285
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PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 12407
LENGTH: 1024
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Publication No. US20030099974A1
                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.0 SEQ ID NO 13285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13285, Application US/09908975 Publication No. US20030165843A1
                                           Matches
                                                              Query Match
Best Local Similarity
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Best Local
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                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SHOSHAN, AVI
APPLICANT: WASSERMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: MINTZ, Eli
APPLICANT: FAIGLER, Simono
TITLE OF INVENTION: OLIOUTULEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2002-07-18
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                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 36688-0005
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ORGANISM: Homo sapiens
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                                                                                                                                                                                 LENGTH: 60
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  14 GCCATCTGCAGGGTCCAGGTGATGG 38
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29; Conservative
                                           Conservative
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100.0%; Pred. No. 6.8
tive 0; Mismatches
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                                                                100.0%;
                                                              19.7%; Score 25; DB 12; 100.0%; Pred. No. 0.0013
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                                           Mismatches
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US-09-764-877-3347
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US-10-198-846-7306
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Best Local S
Matches 21
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                                               SOFTWARE: PatentIn Ver.
SEQ ID NO 3347
LENGTH: 498
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                                                                                                                                                                                                                              GENERAL INFORMATION:
TYPE: DNA
ORGANISM: Homo sapiens
-09-764-877-3347
                                                                                                                                                                           APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PC005
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PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
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TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
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                                                                                                       Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 819, 824, 827, 836, 838, IOCATION: 876, 882, 893, 901, 903, LOCATION: 919, 925, 927, 930, 931 OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 36, 150, 168, 187, 224, 266, 305, 375, 378, 4 LOCATION: 439, 454, 458, 464, 472, 485, 491, 495, 516, LOCATION: 544, 545, 545, 550, 558, 559, 563, 565, 567, LOCATION: 585, 617, 633, 635, 636, 637, 641, 644, 647, OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                   16.5%; Score 21; ilarity 100.0%; Pred. No. Conservative 0; Mismatcl
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812,
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786,
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788,
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5, 536,
7, 570,
7, 651,
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US-10-027-632-113318/c
US-10-027-632-113318/ Application US/10027632
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US-10-027-632-113318
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Best Local (
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SEQ ID NO 113318
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                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                            APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                  PRIOR APPLICATION NUMBER: US 60/193,483 PRIOR FILING DATE: 2000-03-29 PRIOR APPLICATION NUMBER: US 60/185,218 PRIOR FILING DATE: 2000-02-24 PRIOR APPLICATION NUMBER: US 60/167,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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PRIOR FILING DATE: 1999-11-23
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CURRENT FILING DATE: 2002-04-30
                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/198,676 PRIOR FILING DATE: 2000-04-20
                                                                                                                                                                                                                                                          FILE REFERENCE: 108827.129
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APPLICATION NUMBER: US 60/146,002
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FILING DATE: APPLICATION
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Pred. No.
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Pred. No. 1.8;
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US-10-027-632-138349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
GENERAL INFORMATION:

APPLICANT: Wang, David G.

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12
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APPLICANT: Wang, David G.
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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SEQ ID NO 113318
LENGTH: 3372
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Best Local (
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Publication No. US20030204075A9
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Best Local Similarity
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PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
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100.0%; Prr
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100.0%; Pr
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Pred. No.
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APPLICATION NUMBER: US 60/198,676 FILING DATE: 2000-04-20

APPLICATION NUMBER: US 60/193,483

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US-10-027-632-138349
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RESULT 18
US-10-027-632-162983
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; ORGANISM: Human
US-10-027-632-162982
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Best Local
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SEQ ID NO 162982
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Best Local
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PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
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NUMBER OF SEQ ID NOS: 325720
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
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PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
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FILING DATE: 2000-02-24
APPLICATION NUMBER: US 60/167,363
FILING DATE: 1999-11-23
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APPLICATION NUMBER: US 60/146,002
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18; Conserv
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PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
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US-10-027-632-162982
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 162983
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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                           NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 162982
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Matches 18; Conserv
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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CURRENT FILING DATE: 2002-04-30
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                                                            LENGTH: 833
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14.2%;

Score 18;

DB 13;

Length 833;

Best Local Similarity

100.0%;

Pred. No.

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                                                                                                                                                     FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR PILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
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Matches
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LENGTH: 833
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-10-027-632-162983
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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CURRENT FILING DATE: 2002-04-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/218,006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/167,363
FILING DATE: 1999-11-23
APPLICATION NUMBER: US 60/156,358
FILING DATE: 1999-09-28
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FILING DATE: 2000-03-29
APPLICATION NUMBER: US 60/185,218
FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/198,676 FILING DATE: 2000-04-20
                                                                                                    APPLICATION NUMBER: US 60/185,218 FILING DATE: 2000-02-24
        APPLICATION
                                                                                APPLICATION NUMBER: US 60/167,363
                                                                                                                                           FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/146,002
                                             APPLICATION NUMBER: US
                                                             FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 TGTCAAGCTGAAAACAAG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 TGTCAAGCTGAAAACAAG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTCAAGCTGAAAACAAG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTCAAGCTGAAAACAAG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                         60/156,358
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Pred. No.
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7.1;
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US-10-027-632-276727/c
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                                                                                                                                                                                            Sequence 276727, Application US/10027632
Publication No. US20030204075A9
                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                            APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                     CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                  PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12
APPLICATION NUMBER: US 60/198,676
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; ORGANISM: Human
US-10-027-632-31061
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LENGTH: 930
TYPE: DNA
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Best Local S
Matches 18
                                                                                                                                                                                                                   SOFTWARE: FastSEQ
SEQ ID NO 31061
                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 325720
                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
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                                                                                                                                                                             TYPE: DNA
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                                                                                                                                                                                                ENGTH: 930
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                                 108
774 ATTCCTTCCACAACTGCT 791
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                                                                   18;
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                      ATTCCTTCCACAACTGCT 125
                                                                   Conservative
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                                                                                    100.0%;
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                                                                   0,
                                                                                      Score 18; Pred. No.
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                                                                     Mismatches
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                                                                                                    DB 13; Length 930;
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                                                                  Gaps
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RESULT 25
US-09-878-574-2599/c
; Sequence 2599, Application US/09878574
; Patent No. US20020110548A1
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; ORGANISM: Human
US-10-027-632-276727
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US-10-027-632-276727/c
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Best Local
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GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
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CURRENT FILING DATE: 2002-04-30
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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SOFTWARE: FastSEQ for Windows Version 4.0
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les 17; Conserv
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FILING DATE: 1999-11-23
APPLICATION NUMBER: US 60/156,358
FILING DATE: 1999-09-28
APPLICATION NUMBER: US 60/146,002
FILING DATE: 1999-08-09
FILING DATE: 1999-08-09
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FILING DATE: 1999-11-23
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                                                                                                                          51
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                                                                                                                                                                                                                           Similarity
                                                                                                                                                   GCAGGGTCCAGGTGATG 37
                                                                                                                          GCAGGGTCCAGGTGATG 35
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                                                                                                                                                                                               13.4%; Score 17; DB 13;
Llarity 100.0%; Pred. No. 27;
Conservative 0; Mismatches 0
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100.0%; Pr
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Pred. No.
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27;
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; LENGTH: 348
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-023-Q1-B1-B1
US-09-878-574-2599
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US-09-864-761-4974
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PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR PRILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00666
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Best Local :
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CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: Aeomica-X-1
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                                                                                                                              APPLICATION NUMBER: PCT/US01/00662
                                               APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30
                                                                                                          FILING DATE: 2001-01-30
                                                                                                                                                                FILING DATE:
                      APPLICATION NUMBER: PCT/US01/00670
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llarity 100.0%;
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SEQ ID NO 4974
LENGTH: 355
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: Aeomica-X-1
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PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
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                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/207,456 FILING DATE: 2000-05-26
                                                                                                                                                                           FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 09/632,366 FILING DATE: 2000-08-03
                                                                                                            FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
                                                                                                                                           APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: GB 24263.6
                                             APPLICATION NUMBER: PCT/US01/00668
                                                                                              FILING DATE:
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            APPLICATION NUMBER: PCT/US01/00663
                                                                              APPLICATION NUMBER: PCT/US01/00665
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o. US20020048763A1
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Hanzel, David K.
Chen, Wensheng
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Pred. No.
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IN FETAL LIVER, SIGNAL = 1.6

IN BRAIN, SIGNAL = 1.1

IN LUNG, SIGNAL = 1.3

IN HEART, SIGNAL = 1.7

IN HELA, SIGNAL = 1.3

IN HELA, SIGNAL = 1.3

IN ADULT LIVER, SIGNAL = 1.6
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RESULT 28
US-10-066-543-1656
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APPLICANT: Jiang, Yuqiu
APPLICANT: Pyle, Ruth
                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1656
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LENGTH: 355
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Best Local
                                                                                                                                                                 FILE REFERENCE: 210121.563
CURRENT APPLICATION NUMBER: US/10/066,543
CURRENT FILING DATE: 2002-01-31
NUMBER OF SEQ ID NOS: 3417
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PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 60/234,687
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NUMBER OF SEQ ID NOS: 49117
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PRIOR APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                            TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
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NAME/KEY: misc_feature
LOCATION: 211, 453, 454
OTHER INFORMATION: n =
                                                         FEATURE:
                                                                        TYPE: DNA
ORGANISM: Homo
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APPLICATION NUMBER: US 09/608,408
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Indirias, Carol Y
Lodes, Michael J.
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ON: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
ON: EXPRESSED IN HBL100, SIGNAL = 1.5
ON: EXPRESSED IN PLACENTA, SIGNAL = 2
ON: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
ON: EXPRESSED IN BRAIN, SIGNAL = 1.6
ON: EXPRESSED IN LUNG, SIGNAL = 1.3
ON: EXPRESSED IN HEART, SIGNAL = 1.7
ON: EXPRESSED IN HEART, SIGNAL = 1.7
ON: EXPRESSED IN HEART, SIGNAL = 1.6
ON: EXPRESSED IN HEART, SIGNAL = 1.6
ON: NT HIT: AB019786.1, EVALUE 1.20e-01
ON: EST_HUMAN HIT: AA495851.1, EVALUE 2.20e-01
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US-09-918-995-31855
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                         Query Match
Best Local Similarity 100.
Matches 17; Conservative
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PRIOR FILING DATE: 199-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 1344
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Patent No. US20020110548A1
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                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REFERENCE: 20411-756
                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 3.0 EQ ID NO 31855
                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 38054
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                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Glycine max OTHER INFORMATION: Clone ID: LIB3028-039-Q1-B1-E10
                                                                                                                                                                                                                              ENGTH: 500
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15 CCATCTGCAGGGTCCAG 31
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La Rosa, Thomas J.
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                                  Mismatches
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; ORGANISM: Human
US-10-027-632-224793
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US-10-027-632-224793
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GENERAL INFORMATION
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Best Local
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LENGTH: 575
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                                              PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
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SOFTWARE: FastSEQ for
                           NUMBER OF SEQ ID NOS: 325720
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
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CURRENT FILING DATE: 2002-04-30
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CURRENT FILING DATE: 2002-04-30
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PRIOR APPLICATION NUMBER: US 60/146,002
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PRIOR APPLICATION NUMBER: US 60/167,363
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Pred. No.
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RESULT 34
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Best Local S
Matches 17
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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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LENGTH: 712
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Best Local Similarity
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                PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
                                                                                                                     FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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TYPE: DNA
ORGANISM: Human
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FILING DATE: 2000-03-29
APPLICATION NUMBER: US 60/185,218
FILING DATE: 2000-02-24
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NUMBER: US 60/185,218
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                                                           Query Match
Best Local Similarity
Matches 17; Conserv
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SEQ ID NO 255720
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SEQ ID NO 145248
LENGTH: 712
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Publication No. US20030204075A9
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/185,218 PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12
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CURRENT FILING DATE: 2002-04-30
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PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
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                                                                                                                                                                        TYPE: DNA
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                                                                                                                                                                                          ENGTH:
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1695 TTCCTTCCACAACTGCT 1711
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                       TTCCTTCCACAACTGCT 125
                                                                    Conservative
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                                                                                     Score 17; ; Pred. No.
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Pred. No.
                                                                    Mismatches
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                                                                                     . 24;
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25;
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RESULT 36
US-10-027-632-255720
; Sequence 255720, Application
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identif
; TITLE OF INVENTION: Polymo

Application US/10027632

Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

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RESULT 38
US-09-880-107-2295/c
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                                                                         GENERAL
                                                                                         Sequence 2295, Application US/09880107 Patent No. US20020142981A1
                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 3
LENGTH: 2904
TYPE: DNA
ORGANISM: Homo sapien
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LENGTH: 1781
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Publication No. US20030119036A1
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Best Local (
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                     APPLICANT:
                                  APPLICANT: Horne, Darci T. APPLICANT: Vockley, Josep
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CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 60/335,084
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TITLE OF INVENTION: METHODS OF USING 48149, A HUMAN
TITLE OF INVENTION: AMINOPEPTIDASE FAMILY MEMBER
FILE REFERENCE: MPIO1-174P1RM
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NUMBER OF SEQ ID NOS:
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
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CURRENT FILING DATE: 2002-04-30
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                                                                                                                                                                                                         1642
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APPLICATION NUMBER: US 60/185,218
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FILING DATE: 1999-11-23
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                                                                         INFORMATION:
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17; Conserv
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Gene Logic, Inc
                   Vockley, Jos
Scherf, Uwe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.4%; Score 17; DB 13; ilarity 100.0%; Pred. No. 24; Conservative 0; Mismatches 0
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                                  Joseph G.
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                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-31
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Matches
                                                        Matches
                                                                    Query Match
Best Local
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NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
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PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/362,158 PRIOR FILING DATE: 2002-03-05
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CURRENT APPLICATION NUMBER: US/10/205,823
CURRENT FILING DATE: 2002-07-25
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                                                                                                                                                                                                            SOFTWARE:
                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 455
                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/341,746 PRIOR FILING DATE: 2001-12-12
                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR FILING DATE: 2001-09-25
                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/307,982 PRIOR FILING DATE: 2001-07-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
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ORGANISM: Homo sapiens
                                                                                                                                                                        LENGTH:
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17; Conserv
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CCATCTGCAGGGTCCAG
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Gorbatcheva, Bella
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Endege, Wilson O.
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Kamatkar, Shubhangi
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Zhao, Xumei
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                                                  13.4%; Soliarity 100.0%; I Conservative 0;
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100.0%; Pred. No.
tive 0; Mismatc
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                                                                      Score 17; DB 14; 
; Pred. No. 23;
                                                        Mismatches
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1762

CCATCTGCAGGGTCCAG 1746

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Sequence 1, Application US/10281904
Publication No. US20030119036A1
GENERAL INFORMATION:
APPLICANT: Chun, Miyoung
TITILE OF INVENTION: METHODS OF USING 48149, A HUMAN
TITILE OF INVENTION: AMINOPEPTIDASE FAMILY MEMBER
FILE REFERENCE: MPIO1-174PIRM
CURRENT APPLICATION NUMBER: US/10/281,904
CURRENT FILING DATE: 2002-10-28
PRIOR APPLICATION NUMBER: 60/335,084
PRIOR FILING DATE: 2001-10-31
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US-10-281-904-1/c
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CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: US/09/139,802
PRIOR FILING DATE: 1998-08-25
PRIOR APPLICATION NUMBER: 08/926,914
PRIOR APPLICATION NUMBER: 08/710,067
PRIOR APPLICATION NUMBER: 08/710,067
PRIOR FILING DATE: 1997-09-10
PRIOR FILING DATE: 1996-09-10
NUMBER OF SEQ ID NOS: 226
                                                                                           Query Match
Best Local :
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Best Local
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LENGTH: 3494
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APPLICANT: Pasqualini, Renata
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
TITLE OF INVENTION: Same
                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
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LOCATION: (121)..(3024)
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                                                                                                                                                                                                          LENGTH: 3494
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1762 CCATCTGCAGGGTCCAG 1746
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                                                                                             Similarity
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                           CCATCTGCAGGGTCCAG 31
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                                                                           Conservative
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100.0%; Pr
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100.0%; Pr
                                                                       Score 17; DB 14; Length 3494; Pred. No. 23; 0; Mismatches 0; Indels
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RESULT 42

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; FEATURE:
, NAME/KEY: misc_feature
, OTHER INFORMATION: Incyte ID No. US20020160382A1 1344279CB1
US-09-981-353-121
                                                                                                                                RESULT 44
US-10-044-090-218/c
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; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; APPLICANT: Jones, David A.
; TITLE OF INVENTION: GENES EX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-981-353-121/c
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                                                                       Sequence 218, Application US/10044090 Publication No. US20020137081A1 GENERAL INFORMATION:
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SEQ ID NO 221
LENGTH: 3681
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                                                                                                                                                                                                                                                                                                                         Query Match
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CURRENT FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 194
                   TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION FILE REFERENCE: PA-0028 US
                                                     APPLICANT: Olga Bandman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/287,067
PRIOR FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 271
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CURRENT APPLICATION NUMBER: US/10/133,013
CURRENT FILING DATE: 2002-04-25
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APPLICANT: Bandman, Olga
APPLICANT: Cocks, Benjamin G.
TITLE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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CURRENT APPLICATION NUMBER: US/10/044,090
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OTHER INFORMATION: Incyte ID No. US20030166903A1 1136923.19
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100.0%; Pr
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; OTHER INFORMATION: Incyte ID No. US20030119009A1 1344279CB1
US-10-084-817-86
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; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 1344279CB1
US-10-044-090-218
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NUMBER OF SEQ ID NOS: :
SOFTWARE: PERL Program
SEQ ID NO 218
SEQ ID NO 338
                                                                              APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
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LENGTH: 3686
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Publication No. US20030119009A1
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                             PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
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CURRENT FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 60/270,784
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 365
                  SOFTWARE: PatentIn Ver.
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APPLICANT: Jason M. Shohet
TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
FILE REFERENCE: PA-0046 US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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100.0%; Pr
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100.0%; Pr
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Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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; ORGANISM: Homo sapiens
US-09-764-891-6245
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US-09-764-891-6245/c
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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030166903A1 1136923.18
US-10-133-013-222
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                                                     SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6245
LENGTH: 11150
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Best Local Similarity
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SEQ ID NO 222
LENGTH: 3815
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Best Local Similarity
Matches 17; Conserv
                                                                                                            APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrappo NUMBER OF SEQ ID NOS: 10231
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TITLE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE
FILE REFERENCE: PA-0049 US
CURRENT APPLICATION NUMBER: US/10/133,013
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: 60/287,067
PRIOR APPLICATION NUMBER: 60/287,067
PRIOR FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 271
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APPLICANT: Bandman, Olga
APPLICANT: Cocks, Benjami
                                      LENGTH: 11
TYPE: DNA
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NAME/KEY: misc feature
LOCATION: (3707)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
LOCATION: (3713)
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           APPLICANT: Stefansson, Hreinn
APPLICANT: Steinthorsdottir, Valgerdur
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001
CURRENT APPLICATION NUMBER: US/09/795,668
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/515,716
PRIOR FILING DATE: 2000-02-28
                                                                                                                                                                                                                                          US-09-795-668-1
                                                                                                                                                                                                                                                             RESULT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-428-561
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                                                                                                                                                                                 Sequence 1, Application US/09795668 Patent No. US20020045577A1 GENERAL INFORMATION:
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SEQ ID NO 561
LENGTH: 11150
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GENERAL INFORMATION
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CURRENT FILING DATE: 2002-07-26
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NUMBER OF SEQ ID NOS: 1019
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PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
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PRIOR FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PA117C1
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/214,886
FILING DATE: 2000-06-28
APPLICATION NUMBER: 60/217,487
FILING DATE: 2000-07-11
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Search completed: November Job time: 491.785 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                           Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 263)
1 (Case http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
                                                                                                                                                                                                                                                                                                                BE624166 263 bp mRNA linear EST 24-AUG-2000 uu42d01.yl Soares mammary_gland_NMLMG Mus musculus cDNA clone IMAGE:3374593 5' similar to WP:R10A10.2 CE12670 ZINC FINGER PROTEIN
                High quality sequence stop:
Location/Qualifiers
                                           Seq primer: -40RP from Gibco
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Tissue Procurement: Dr. Leslie L. Heckert
                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 291)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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CB570887.1 GI:29490417
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291 bp
AGENCOURT 13009672 NIH MGC 165 Mus
IMAGE: 30276894 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CB570887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     musculus (house mouse)
                                                                                                                                                                               quality sequence stop: 291.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Soares_mammary_gland_NMLMG"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo. "
a 61 c 77 g 61 t
                    /tissue_type="primary cultures of Sertoli
/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="NIH_MGC_165"
                                                                                clone="IMAGE:30276894"
                                                                                                                                      organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
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/tissue_type="mammary gland"
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                                                                                                   xref="taxon:10090"
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                                                                                                                        _type="mRNA"
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Pred. No. 1.7e-55;
; Mismatches 0;
    testis;
Vector: pDNR-LIB; Site_1: Sfil
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s cDNA clone
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RESULT 2 CB570887

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KEYWORDS VERSION ACCESSION

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RESULT 3
AA231201
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127; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 296)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T. Geisel,S., Kucaba,T., Lacy,M., Le,M., Marrin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA231201

296 bp mRNA linear EST 26-FEB-mw38g11.rl Soares mouse 3NME12 5 Mus musculus cDNA clone
IMAGE:673028 5' similar to WP:ZK287.5 CE06614 ;, mRNA sequence.
                                                                                                                                                                                                                                                                                   IMAGE Consortium (info@image.llnl.gov)
MGI:412732
                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                      4444 Forest Park Parkway, Box 8501,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                              Seq primer: -28m13 rev2 ET from
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                                                                                                                                                                                                                                         quality sequence stop: 258
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                /tissue_type="fetus"
/dev_stage="12.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                 /mol
                                                                                                                                       /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                  organism="Mus musculus"
                                                                                sex="unknown"
                                                                                                 clone="IMAGE: 673028"
                                                                                                                    db_xref="taxon:10090"
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_lib="Soares mouse 3NME12 5"
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Pred. No. 1.7e-55;
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ACCESSION
VERSION
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Best Local S
Matches 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BE624155 303 bp mRNA linear EST 24-AUG-2000 uu42c01.yl Soares_mammary_gland_NMLMG Mus musculus cDNA clone IMAGE:3374592 5' similar to WP:R10A10.2 CE12670 ZINC FINGER PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 303)
NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE624155.1 GI:9904571
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                       primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                        quality sequence stop: 292.
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/clone ib="Soares mammary gland_NMLMG"
/note="Vector: pT773D-Pac (Pharmacia) with a modified
polylinker; lst strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo. "
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/mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                                                                      /clone="IMAGE:3374592"
/sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
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Pred. No. 1.7e-55;
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                                                                              cDNA was
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RESULT 4 BE624155

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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu, Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA000941 309 bp mRNA linear EST 18 mg36b06.rl Soares mouse embryo NbMEl3:5 14.5 Mus musculus clone IMAGE:425843 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                     Seq primer: ETPrimer High quality sequence
                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                        Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Location/Qualifiers
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/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                       /clone="IMAGE: 425843"
/sex="unknown"
                                                                                                                                                                                                                                                             organism="Mus musculus"
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No. 1.7e-55;
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                                                                                                                                                                                                                        Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J. A., Badla, E., Dragani, T. A., Fletcher, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustinoich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, W., Jackson, I. J., Pertea, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Resole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Resole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Redole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Redole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Redole, G., Wang, Y., Watanabe, Y., Wallana, R., Takenaka, Y., Taylor, M.S., Teasdale, M., Sahama, K., Varagisawa, M., Varagi, I., Yuan, Z., Zavolan, M., Zhaylor, M.S., Teasdale, M., Sakazume, N., Satok, Shiraki, T., Waki, K., Kawai, J., Nakamura, M., Sakazume, N., Satok, Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, M., Imara, A., Hashizume, M., Imara, K., Shibata, K., Shibata, K., Shibata, K., Shibata, J., Alawa, K., R., Shibata, J., Alawa, K., R., Shibata, J., Alawa, K., R., Shibata, J., Shibata, J., Shibata, J., Shibata, J., Jaha, J., J
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                     Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suphiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jag
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                                                                                                                                                                                       Nature 420, 563-573 (2002) 22354683
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          22 Suehiro-cho,
81-45-503-9222
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Pred. No. 1.7e-55;
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                                                                                                                                                                       musculus
BY329058
Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 319)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs t prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prepare mouse tissues. Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece ) whose assistance we gratefully
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                further details.
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URL:http://genome.gsc.riken.go.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Murata,M., Nakamura,M., Sato,K., Shibata,K., Shiraki,T., Tagami
, Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
, Makki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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Email: genome-res@a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                      CIGCIGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Computational Analysis of Full-Length Mouse cDNAs Compared with uman Genome Sequences Mamm. Genome. 12, 673-677 (2001)
                                                                                                   musculus
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
,Murata,M., Nakamura,M., Nomura,K., Nhumazaki,R., Ohno,M., Sakai,K., Sahazaume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,
,M., Maki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                   prepare mouse tissues.

Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece ) whose assistance we gratefully acknowledge.
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                                                                                                                                                                         further details.
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Normalization and subtraction of cap-trapper-selected
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                                                                                                                                                                                                                  Please visit our web site (http://genome.gsc.riken.go.jp) for
organism="Mus musculus"
                                                                                                               Socation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 321)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Duby, Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B. Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      w78263
                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chòrdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                         quality sequence stop: 306
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="L130007G07"
/cell_type="synovial fibroblasts"
/clone_lib="RIKEN full-length enr.
fibroblasts"
85 c 102 g 67 t
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                         <u>a</u>b
                                                                                                                                                               'sex="unknown"
                                                                                                                                                                                                                          strain="C57BL/6J"
                                                                                                                                                                                                                                                                   organism="Mus musculus"
                                                                                                                                                                                    clone="IMAGE:401827"
                                                                                                                                                                                                         xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Louis,
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JOURNAL
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                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                   Nikaido, I., Osato, N., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustinoich, S., Hirokawa, N., Jackson, I. J., Jarvis, D.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., Jarvis, B.D., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchiomni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., P.A., Maglott, D.R., Naltais, L., Marchiomni, L., McKenzie, L., Miki, Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.E., Kingwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y. Taylor, M.S., Tessdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watshaw, B., Yang, I., Yang, L., Yang, L., Yang, L., Sanda, M., Yanjaisawa, M., Yang, I., Yang, L., Yang, L., Wahlestedt, C., Wang, Y., Waki, K., Sakazume, N., Sakazi, D., Shibata, R., Sakazi, D., Shibata, S., Haras, A., Hashizume, W., Imotani, K., Ishii, X., Ishii, Sakasi, J., Sakazi, D., Shibata, S., Barney, E. and Hayashizaki, Y., Sakazi, D., Shibata
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                                                                            Analysis of the mouse transcriptome of 60,770 full-length cDNAs Nature 420, 563-573 (2002)
                                                        Nature 420,
22354683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY125373 RIKEN full-length enriched, adu
CDNA Clone L630036A16 5', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Pred. No. 1.7e-55;
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Contact: Yoshihide Hayashizaki

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ORIGIN
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Best Local
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         127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prepare mouse tissues.

Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
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URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Alzawa,K., Akimura,T., Arakawa,T., Carninci,D., Konno,H., Miyazaki,A.,
T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,M., Sakai,K.,
Murata,M., Nakamura,M., Nomura,K., Nhibata,K., Shiraki,T., Tagami,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Sh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Normalization and subtraction of cap-trapper-selected prepare full-length cDNA libraries for rapid discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submission
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    Conservative
                                                                                                                                                                                                                             70
                                                                                                                                                                                                                                                                                                                                              /clone lib="RIKEN full-length enriched, adult male brain"
/note-"Site 1: Sall; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified pBluescript
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            db_xref="taxon:10090"
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                                             100.0%;
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                                                                                                                                                                                                                         Ω
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    0
                                             Score 127; DB 13;
Pred. No. 1.7e-55;
    Mismatches
                                                                                                                                                                                                                    ω
                                                                                                                                                                                                                                                                                                          KS(+) after bulk excision from Lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mouse tissues. 1st strand cDNA was
    Indels
                                                                                     Length 322;
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Gaps
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RESULT 11
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Best Local
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BE692680
BE692680.1 GI:10080304
EST.
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Seq primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
Other_ESTs: uw44b12.x1
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1 (Dases 1 to 323)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE692680 323 bp mRNA linear EST 11-SEP-2000 uw44b12.yl Soares mammary_gland_NMLMG Mus musculus cDNA clone IMAGE:3464831 5' similar to WP:R10A10.2 CE12670 ZINC FINGER PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                            Similarity
                                                                    CTGCTGC 251
                                                                                                    CTGCTGC 127
                                                                                                                                     TGAMAACAAGCAAGAGGACTGTTGTTGTGGTCTGGGGAGAGTGTAACCATTCCTTTCCACAA
                                                                                                                                                          GTGCGATACCTGTGCCATCTGC
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Location/Qualifiers
                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                73
                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Soares mammary_gland_NMLMG"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo. "
a 80 c 102 g 68 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:3464831"
/sex="female (lactating)"
/tissue_type="mammary gland"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                      Score 127; DB 10;
Pred. No. 1.7e-55;
; Mismatches 0;
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JOURNAL
                                                                                                                                                                                                                                                                                                              Best Local Similarity
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141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 325)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN SAG. ;, mRNA sequence.
BF012987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGI:1417389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Marra M/WashU-NCI Mouse EST Project 1999
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                                                         // Lab_host="blub" (phage-resistant)"
// Lab_host="blub" (phage-resistant)
// 
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/lab_host="DH10B (
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                           Score 127; DB 10;
Pred. No. 1.7e-55;
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                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                           COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                             176
                     121
                                                                                                                                       127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA623723

328 bp mRNA linear EST 14-OCT-1
vg72g03.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone
vg72g1107892 5' similar to WP:ZK287.5 CE06614 ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA623723.1 GI:2527599
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
1 (bases 1 to 328)
CTGCTGC 127
                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                           76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 263.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                /note=Torgan: embryo; Vector: pBluescribe (modified); Site 1: MluI; Site 2: SalI; Cloned unidirectionally from mRNA prepared from 13:500 2-cell stage embryos. Primer: SalI(dI): 5'-CGGTCGACCGTCGACCGTTTTTTTTTTTTT-3'. cDNA were cloned into the MluI/SalI sites of a modified pBluescribe vector using commercial linkers (NEB). Average insert size: 1.2 kb."

a 78 c 104 g 70 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reversed clone: similarity on wrong strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="embryo"
/dev_stage="2-cell"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/strain="C57BL/6J x DBA/2J F1"
/db xref="reaxon:10090"
/clone="IMAGE:1107892"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone_lib="Knowles Solter mouse 2 cell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207
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                                                                                                                                                                                                                   100.0%; Score 127; DB 9; 100.0%; Pred. No. 1.7e-55; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                            Length 328;
                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST 14-OCT-1997
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                                                           235
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SOURCE ORGANISM
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BY342015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
MEDLINE
PUBMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nikaido, I. Osato, N. Satto, R. Suzuki, H., Yamanaka, I. Kyosawa, H. Nikaido, I. Osato, N. Satto, R. Suzuki, H., Yamanaka, I. Kyosawa, H. Yagi, K., Tomaru, Y., Hasegawa, Y. Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gastierland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., P.A., Maglott, D.R., Maltais, L., Marchiomi, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, M., Sahama, J., Wan, J., Yang, L., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., M., Sakazume, N., Sato, K., Shiraki, T., Wahlsetedt, C., Wang, Y., Wang, L., Yang, L., Milming, L.G., Wynshaw-Boris, A., Yanagisawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Ishii, Y., Ishii, Y., Ishii, Y., Ishii, M., Kayawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y. Sasaki, D., Shibata, G., Shipataki, Y., Sasaki, D., Shibata, S., Hara, S., Shinada, Y., Manda, Y., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Shipata, S., Shipataki, Y., Sasaki, D., Shibata, S., Hara, S., Shipataki, Y., Sasaki, D., Shibata, S., Shipataki, Y., Sasaki, D., Shibata, S., Shipata, S
Normalization and subtraction of cap-trapper-selected cDNAs prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                            Email: genome-res@gsc.riken.go.jp,
URLihttp://genome.gsc.riken.go.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
T., Imotani,K., Ishi,Y., Itoh,M., Kawai,J., Konno,H., Miy
, Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M.,
, Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T.,
,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1-7-22 Suehiro-cho,
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                                                                                                                                                                                                                                              Human Genome Sequences Mamm.
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                                                                                                                                                                                                                                          Computational Analysis of Full-Length Mouse cDNAs Compared with Luman Genome Sequences Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 328)
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Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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                                                                                                                                                                                                    cDNAs to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hirozane
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sakai,
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encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

Computer-based methods for the mouse full-length cDNA

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SOURCE
ORGANISM
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BY114710
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Best Local Simi
Matches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
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Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pestovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, R.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zinmer, A., Kahmura, K., Nakamura, K., Kahikawa, T., Konno, H., Nakamura, A., Sahmura, K., Nakamura, K., Na
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BY114710
BY114710.1 GI:26225811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY114710 329 bp mRNA linear EST 08-DEC-200: BY114710 RIKEN full-length enriched, 18 days embryo whole body Mus musculus cDNA clone L430031L17 5', mRNA sequence.
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Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari,Greece ) whose assistance we gratefully
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Okazaki,Y., Furuno,M.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/mol_type="mRNA"
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length CDNA libraries for rapid discovery of new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: genome-res@gsc.riken.go.jp,
URL:hhtp://genome.gsc.riken.go.jp/
URL:hhtp://genome.gsc.riken.go.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishi,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
T., Imotani,K., Ishi,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
M., Matani,K., Nakamura,M., Nomura,K., Nhinaki,T., Tagami,
Sato,K., Shizaki,T., Tagami,
M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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The Institute of Physical and Chemical Research (RIKEN)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
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Fax: 81-45-503-9216
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/tissue_type="whole body"
/dev_stage="18 days embryo"
/clone_libe="RIKEN_full-length
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BY337380 346 bp mRNA BY337380 RIKEN full-length enriched, whole clone L230006P10 5', mRNA sequence.
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Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

1 (basse 1 to 332)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
This clone is available royalty-free t.
TMAGE Consortium (info@image.llnl.gov)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4444 Forest Park Parkway, Box 8501, St. Louis, MO Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA110259
33 bp mRNA linear EST 02-OCT-1997
mp07g09.rl Life Tech mouse embryo 8 5dpc 10664019 Mus musculus cDNA
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Fax: 314 286 1810
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/note="Organ: whole embryo; Vector: pcMV-SPORT2; Site_1:
SalI; Site_2: NotI; Cloned unidirectionally. Primer:
Oligo dT. 8.5dpc embryos. pcMV-SPORT2 vector."
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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/dev_stage="8.5dpc embryos"
/lab_host="DH10B"
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encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece ) whose assistance we gratefully
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozan,T., Imotani,K., Ishi,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,J., T., Imotani,K., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,J., Murata,M., Nakamura,M., Nomura,K., Shibata,K., Shiraki,T., Tagami,Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,Y., Direct
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The Institute of Physical and Chemical Research (RIKEN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H.,
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Best Local :
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                                                  Nikaido, I. Osato, N. Saito, R., Suzuki, H., Yamanaka, I., Kyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bull, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J. A., Bradt, D., Brusic, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, P. A., Maglott, D.R., Nanta, K., Okido, T., Pavan, W. J., Pertea, G., P. A., Magsahima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G., B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Varardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Arakawa, T., Konno, H., Nakamura, K., Arakawa, T., Kayawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Haysahizaki, Y.
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EST.
Mus musculus (house mous
Mus musculus
                Analysis of the mouse transcriptome based on functional annotation of 60,770 full_length cDNAs
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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RIKEN full-length enriched, 15 days embr
cDNA clone L330005N21 5', mRNA sequence
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/clone="L230006P10"
/tissue_type="whole joints"
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/clone_Tib="RIKEN full-length enriched, whole joints"
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Pred. No. 1.8e-55;
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BY116440 RIKEN full-length enriched, 18 days embr
musculus cDNA clone L430049B20 5', mRNA sequence
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BY116440 GI:26227541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
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URL:http://genome.gsc.riken.go.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P.,
T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Ko
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/clone_lib="RIKEN full-length
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/mol_type="mRNA"
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/clone="L330005N21"
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SOURCE
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                                                                                                                                                                                                                                             encyclopedia: real-time sequence clustering for construction of a nonredundant CDNA library. Genome Res. 11 (2), 281-289 (2001) CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Re 10 (11), 1757-1771 (2000)
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
                                                                                                                                                                                                             Division of Experimental Animal Research in Riken contributed to
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URL:http://genome.gsc.riken.go.jp/
Alzawa,K. Akimura,T. Arakawa,T. Carninci,P., Fukuda,S., Hirozane
Alzawa,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Nhumazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,
M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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                                                                                                                                             Nikaido, I., Saato, N., Saato, R., Suzuki, H., Yamanaka, I., Kyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schimil, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Kamai, A., Kawaji, H., Kawasawa, Y., Kedzlerski, R.M., Varvis, E. D., Kanai, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, M., M., Salb, L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagshima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Percrovsky, N., Pillai, R., Pontius, J.U., Oi, D., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Oi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.J., Kingwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shinada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Wals, J., Yang, I., Yang, J., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., M., Yang, I., Yang, L., Yang, L., Wahlestedt, T., Waki, K., Kawai, J., Nakamura, K., Shinada, K., Shin
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,K., Shinagawa,A., Yasunishi,A., Yosuniu,m., muccome, E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 351)
Okazaki,Y., Furuno,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY170257 RIKEN full-length enriched, bone marrow musculus cDNA clone 1830081B12 5', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
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/dev stage="18 days embryo"
/clone lib="RIKEN full-length enriched, 18 days embryo
whole body"
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/strain="C57BL/6J"
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Pred. No. 1.8e-55;
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PUBMED COMMENT

Yoshihide Hayashizaki

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RESULT 20
BY091208
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Best Local
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BY091208
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musculus
BY091208
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Tissues were provided by David A. Hume ( Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia ) whose assistance we gratefully acknowledge.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-Length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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URL:http://genome.gsc.riken.go.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Alzawa,K., Ishi,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
T., Imotani,K., Ishi,Y., Itoh,M., Xawai,J., Konno,M., Sakai,K.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Murata,M., Wakai,K., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Division of Experimental Animal Research in Riken contributed to prepare mouse tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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                        352 bp m
RIKEN full-length enriched,
cDNA clone K630085B17 5', m
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a 93 c
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/clone="1830081B12"
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Pred. No. 1.8e-55;
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VERSION
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MEDLINE
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                                                                                                                                                                                                 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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URL:http://genome.gsc.riken.go.jp/
Rizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Aizawa,K., Akimura,T., Arakawa,T., Carninci,D., Konno,H., Miyazaki,A.,
T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Nhumazaki,R., Ohno,M., Sakai,K.,
Sakazume,JN., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,K.,
Sakazume,JN., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,K.,
Maki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Nikaido,I., Osato,N.,
                                   further details.
                                                                      prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp)
                                                                                                                                                         Division of Experimental Animal
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Location/Qualifiers
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Saito, R., Suzuki, H.,
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                                                                                                                                                                  in Riken contributed
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                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Ana
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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h quality sequence stop: 
Location/Qualifiers
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/clone 11.
whole body"
86 c
T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized; constructed by Bento Soares and M.Fatima Bonaldo."

8 3 c 111 g 76 t
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/tissue_type="middle body"
/dev_stage="13 days embryo"
/clone_lib="RIKEN full-length enriched, 13 days embryo
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/db_xref="taxon:10090"
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. No. 1.8e-55;
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BY090965
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                                                                                                                                                                                                                                                                 NKE (Dases 1 to 357)

NKASUKA, Y. Puruno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D., P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, C., Goggh, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ring, B.Z., Rayasi, T., Reed, J.C., Reed, D.J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wanner, L., Wahlestedt, C., Wang, Y., Wanabe, Pontius, J., Yang, I., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, Y., Analysis of the mouse transcriptome based on functional annotation of 60,700 full-length cDNAs
BD 1246681
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T.,
                                                                                                   1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
                                                                                                                        Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jan
                                                                                                                                                                                                                            Contact: Yoshihide Hayashizaki
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musculus cDNA clone K630083012 5', mRNA sequence
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Carninci, P.,

Fukuda, S., Hirozane

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RESULT 23
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                                                                                                                  AUTHORS
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Eukaryota; Me
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 361)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, I., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S.,
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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/dev_stage="13 days embryo"
/clone_lib="RIKEN full-length enriched, 13
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="K630083012"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prepare mouse tissues.

Tissues were provided by Michelle Brinkmeier and Sally Camper (
Dept. Human Genetics University of Michigan Medical School 4301
MSRB 3 1500 W. Medical Center Ann Arbor, MI 48109-0638 USA)
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new
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URL:http://genome.gsc.riken.go.jp/
URL:http://genome.gsc.riken.go.jp/
Alizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Alizawa,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,M., Sakai,K.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
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22354683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          whose assistance we gratefully acknowledge. Please visit our web site (http://genome.c
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/tissue_type="Rathke's pouches"
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/clone_lib="RIKEN full-length enriched,
df/df Rathke's pouches"
                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Ld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA403365 366 bp mRNA linear ES: va33a04.rl GuayWoodford Beier mouse kidney day 7 Mus mu clone IMAGE:733134 5' similar to WP:ZK287.5 CE06614 ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T. Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
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                                                           /tissue_type="kidney"
/dev_stage="juvenile (7 days old)"
/dev_stage="juvenile (7 days old)"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="GuayWoodford Beier mouse kidney day 7"
/clone_lib="GuayWoodford Beier mouse kidney day 7"
/note="Organ: kidney; Vector: pBluescript SKr, Site 1:
/note="Organ: kidney; Vector: pBluescript SKr, Site 1:
/note="Organ: kidney; Vector: pBluescript SKr, Site 1:
/note="Organ: kidney; Vector: pBluescript Skr, primer:
/note="Organ: kidney; Vector: pBluescript Skr, primer:
/note="Organ: kidney; Vector: pBluescript Skr, primer:
/note="Organ: pBluescript Skr, primer: pBluescript Skr, primer:
/note="Organ: pBluescript Skr, pBluescript
                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="C57BL/6J"
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Ld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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5′ similar
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Location/Qualifiers
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Fax: 314 286 1810
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Conservative (
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                                                                                                                       provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                clone="IMAGE:582619"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                  tissue_type="Thymus"
                                                                                                                                                                                                                                                                                                                                                                                          sex="male"
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
,Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.
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                                                                                                                                                                                     Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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BY089817.1 GI:26204179
EST.
                                                                                                                                                                   1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                   Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)
                                                                                                                                                                                                                                                                                               Contact: Yoshihide Hayashizaki
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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full-length enriched, 10 days neor
clone K630078H15 5', mRNA sequence.
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Pred. No. 1.8e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
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d, 10 days neonate
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mu
1 (bases 1 to 371)
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BY091920 RIKEN full-length enriched, pooled tissues, adult
etc. Mus musculus cDNA clone K630089C13 5', mRNA sequence.
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10 (11), 1757-1771 (2000)
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RIKEN integrated sequence analysis (RISA) system--384-format
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M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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/dev_stage="10 days neonate"
/clone_lib="RIKEN full-length
brain"
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/strain="C57BL/6J"
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Pred. No. 1.8e-55;
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Godzik, A
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King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons
, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki
, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G.,
Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D.,
Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Ring
, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou
, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale
, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y.,
Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa
, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A.,
Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura
, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii
, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata
, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander
, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome in Riken Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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URL:http://genome.gsc.riken.go.jp/
Aizawa,K. Akimura,T. Arakawa,T. Carninci,P., Fukuda,S., Hirozane
Aizawa,K., Ishi,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
T., Imotani,K., Ishi,Y., Itoh,M., Kawai,J., Konno,M., Sakai,A.,
Murata,M., Nakamura,M., Nomura,K., Nhumazaki,R., Ohno,M., Sakai,K.,
Sakazume,M., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,
M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 420, 563-573
22354683
12466851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Computational Analysis of Full-Length Mouse cDNAs Compared with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gough, J., Grimmond, S.,
/clone_lib="RIKEN full-length enriched, pooled tissues, adult spleen, etc."
/note=""(dev_stage=adult,tissue_type=spleen,sex=male),
(dev_stage=adult,tissue_type=kidney,sex=male),
(dev_stage=adult,tissue_type=thymus,sex=male),
(dev_stage=adult,tissue_type=thymus,sex=male),
(dev_stage=adult,tissue_type=eatut,sex=male),
(dev_stage=adult,tissue_type=colon,sex=male),
(dev_stage=adult,tissue_type=stomach,sex=male),
(dev_stage=adult,tissue_type=stomach,sex=male),
(dev_stage=adult,tissue_type=liver,sex=male),
(dev_stage=adult,tissue_type=liver,sex=male),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="K630089C13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _xref="mRNA"
_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jackson, I.J.,
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COMMENT MEDLINE

PUBMED

JOURNAL TITLE

FEATURES

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RESULT 28
BY169149
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KEYWORDS
    COMMENT
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                                                                                                   JOURNAL MEDLINE
                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                      PUBMED
                                                                                                                                 King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, D.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teaddale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, B.S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 CTGCTGC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Lenhard, B., Lyons
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BY169149 RIKEN full-length enriched, bone marrow musculus cDNA clone I830074N02 5', mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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                                                      12466851
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RESULT 29
BY172672
                                                                                         DEFINITION
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Best Local
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BY172672
BY172672
musculus
BY172672
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Tissues were provided by David A. Hume ( Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia ) whose assistance we gratefully acknowledge.
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URL:http://genome.gsc.riken.go.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new
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RIKEN integrated sequence analysis (RISA) system--384-format
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                                                  Nikaido, I., Osato, N., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Belsel, K. W., Blake, J. A., Bradt, D., Brusic, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kurochkin, I. V., Lee, Y., Lehard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Percea, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Kingwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanaba, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yana, Z., Zavolan, M., Zhu, Y., Zimmer, A., M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Kogers, J., Birney, E. and Hayashizaki, Y.

Alalysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
                                     Nature 420,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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COMMENT JOURNAL MEDLINE PUBMED

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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P.,
,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., K

Submission Computational Analysis of Full-Length Mouse cDNAs Compared with Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai, Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami, Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Konno, H., Miyazaki, A. Sakai, K.

prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000) Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to

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Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riker. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed

and Microbiology/Parasitology Institute i University of Queensland Brisbane,Q 4072 assistance we gratefully acknowledge. prepare mouse tissues.

Tissues were provided by David A. Hume ( Depts. of Biochemistry for Molecular Australia )

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        Quackenbush, J. Schritml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldd, M., Gissi, C., Godzik, A., Frazer, K.S., Gaasterland, T., Gariboldd, M., Gissi, C., Godzik, A., Gough, J., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pertovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Konno, H., Nakamura, K., Sakati, D., Sato, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y., Sakati, D., Shibata, K., Shisasi, Set the mouse transcriptome based on functional annotation
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Nikaido, I., Osato, N.,
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cDNA clone I830035A17 5', mi
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/cell_type="macrophage"
/clone_lib="RIKEN full-length enriched, bone marrow
macrophage"
a 99 c 122 g · 75 t
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/clone="1830094D24"
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pred. No. 1.8e-55
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prepare mouse tissues.

Tissues were provided by David A. Hume ( Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience university of Queensland Brisbane, Q 4072 Australia ) whose university of Queensland Brisbane, Q 4072 Australia ) whose assistance we gratefully acknowledged acknow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
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Nature 420, 563-573 (2002)
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Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hiroza,T., Imotani,K., Ishi,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,, Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai, Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami, Sakazume,N., Sasaki,A., Muramatsu,M. and Hayashizaki,Y. Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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/mol_type="mRNA"
276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="bone marrow"
/cell_type="macrophage"
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Ohno, M., Sakai, K.
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Nikaido, 1. Osato, N. Saito, R., Solo, H., Kondo, S.,
Nikaido, 1. Osato, N. Saito, R., Schonbach, C.,
Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A.,
Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A.,
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Pallake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani
L.E., Cousins, S., Dallake, E., Dragani, T.A., Fletcher, C.F., Forrest
A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A.,
Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J.,
Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M.,
King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons
P.A., Maglott, D.R., Maltais, L., Marchiomni, L., McKenzie, L., Miki
H., Nagashima, T., Numata, K., Okido, T., Pavan, M.J., Pertea, G.,
Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D.,
Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring
B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou
M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale
R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y.,
Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yangaiswa
M., Yang, L., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zammer, A.,
M., Yang, L., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zammer, A.,
M., Yang, L., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zammer, A.,
M., Yashawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii
N., Y., Itoh, M., Kagawa, J., Miyazaki, A., Sakai, K., Sasaki, D., Shibata
R., Shinagawa, J., Shibata
Native, A., Native, A., Native, Shibata
Native, A., Native, Shibata
Native, A., Shibata

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                               sequencing
10 (11), 17
                                                                                                                                                                                                                                                                                                             Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs |

prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format
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Laboratory for Genome Exploration Research Group, RIKEN
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sabazume,M., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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BY307739 RIKEN full-length enriched, stroma cell Mus musculus cDNA clone 1320001102 5', mRNA sequence.
BY307739 GI:26498076
EST.
Mus musculus (house mouse)
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Fax: 81-45-503-9216
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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1757-1771 (2000)
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National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdnæ8lgsun.grc.nia.nih.gov
Plate: B0492 row: H column: 01
Seq primer: M13 Reverse
High quality sequence stop: 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H. Construction of long-transcript enriched cDNA librarie submicrogram amounts of total RNAs by a universal PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 393)
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                                                                                                                                                                                                                                                                                                                                                             Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                                                                                                                      11544199
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Tissues were provided by Takashi Ishikawa ( Department of Surgery 2 Yokohama City University 3-9 Fukuura, Kanazawa-ku, Yokohama 236-0004 Japan ) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                                                                                                                                                  Location/Qualifiers
clone="NIA:B0492H01 IMAGE:30447540"
/tissue_type="E6.5 whole embryo"
                                         db_xref="niaEST:B0492H01-5"
db_xref="taxon:10090"
                                                                                   /mol_type="mRNA"
/strain="C57BL/6J"
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/clone_lib="RIKEN full-length enriched, stroma cell"
103 c 129 g 80 t
                                                                                                                               'organism="Mus musculus"
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/db_xref="taxon:10090"
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Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Mikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegaway,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothai,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustinoich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from 0.53 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.3kb. The library was constructed by Yulan Piao."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://gsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001) [PMID: 11544199]). Total RNAs were extracted from a pool of 7 embryos at 6.5-days postcoitum. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev stage="whole embryo including extraembryonic tissues
at 6.5-days postcoitum"
/lab_host="DH10B"
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RESULT 33

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BASE COUNT

REFERENCE

AUTHORS

8

ORIGIN

KEYWORDS ACCESSION DEFINITION

ORGANISM

VERSION

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BASE COUNT
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           Matches 127;
                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissues were provided by Michela Fagiolini and Takao K. Hensch (Laboratory for Neuronal Circuit Development Brain Science Institute RIKEN 2-1 Hirosawa, Wako-shi, Saitama 351-0198 Japan ) whose assistance we gratefully acknowledge. Please visit our web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    assistance we gratefully acknowledge. Please (http://genome.gsc.riken.go.jp) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
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22354683
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           Conservative
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                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="K430330L01"
/tissue_type="visual cortex"
/tissue_type="visual cortex"
/clone_Tib="RIKEN full-length enriched, visual cortex"
/clone_Tib="RIKEN full-length enriched, visual cortex"
/clone_Tib="10 g 82 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                           /mol
                                                                                                                                                                                                                                                                                                                                                                     mol_type="mRNA"
strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                      100.0%;
       °.
Score 127; UB 11,
Pred. No. 1.8e-55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nikaido, I., Saato, N., Saito, R., Suzuki, H., Yagi, K., Tomaru, Y., Batchard, I., Kyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schbriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gassterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lehnard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Oi, D., Reid, J., Ring, R., Rawasi, T., Reed, J.C., Reed, D.C., Reid, J., Ring, R., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanaba, Y., Wang, E., Wagner, L., Wahlestedt, C., Wang, Y., Watanaba, Y., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., M., Sakai, M., Sakai, M., Sakai, M., Sakai, J., Aizawa, K., Arakawa, T., Konno, H., Nakamura, K., Shinadawa, Y., Kamai, J., Aizawa, K., Arakawa, T., Kayawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinada, Y., Bairney, E. and Hayashizaki, Y. Saski, D., Shibata, K., Shinada, Y., Bairney, E. and Hayashizaki, Y.

Palaysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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                                                                                                               Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Aizawa,K., Ishi,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
T., Imotani,K., Ishi,Y., Itoh,M., Kawai,J., Konno,M., Sakai,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,
M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
                                                                                                                                                                                                                                                                                                                                                      Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Computational Analysis of Full-Length Mouse cDNAs Compared with fuman Genome Sequences Mamm. Genome. 12, 673-677 (2001) Normalization and subtraction of cap-trapper-selected cDNAs to
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AUTHORS
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Matches 127;
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Best Local
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BG277656.1
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                                                                                                                            Other_ESTs: ux47c07.x1
Contact: Robert Strausberg,
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                  Mammalia; Eutheria; Rodentia; Sciurognathi; M
1 (bases 1 to 397)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ux47c07.y1 Soares_NMMAX_maxillary_process Mus musculus cDNA c.
IMAGE:3513229 5' similar to TR:Q9WTZ1 Q9WTZ1 ZINC RING FINGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Computer based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
                                                               MGI:1393805
                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                Unpublished
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                           Seq primer: -40RP from Gibco
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RIKEN integrated sequence analysis (RISA) system--384-format
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quality sequence stop:
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="whole body"
/dev stage="17 days embryo"
/clome_lib="RIKEN full-length enriched, 17 days embryo
whole_body"
97 c 128 g 81 t 1 others
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/strain="C57BL/6J"
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Pred. No. 1.8e-55;
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; Murinae; Mus
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AUTHORS
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                                                         High
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAtional Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                 401 bp mRNA linear EST 06-OC us40e01.yl Soares NMEBA branchial arch Mus musculus cDNA clon IMAGE:3169560 5' similar to TR:Q9WTZ1 Q9WTZ1 ZINC RING FINGER
                                                                      Seq
                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M.
                                                                                    MGI:1065020
                                                                                                          image.llnl
                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                         Mus musculus
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                                                                                                                      DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be cound through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                        cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                            quality sequence stop: :
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:10090"
                    organism="Mus musculus
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/mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                          .gov/image/html/iresources.shtml
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Pred. No. 1.8e-55;
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JOURNAL
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Best Local
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194 TGAAAACAAGCAAGAGGACTGTGTTGTGGTGGGGAGAGTGTÄACCATTCCTTCCACAA
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                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 409) Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu. Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W34101 409 bp mRNA linear EST 11-SEP-1 mb01c09.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:318928 5' similar to WP:F35G12.9 CE00978 ;, mRNA sequence.
                                                                                                                                                                                                                                 Conflact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GTGCGATACCTGTGCCATCTGCAGGGTCCAGGTGATGGCTGCCTTCGATGTCAAGC 60
                                                                                                             Seq primer: ETPrimer
                                                                                                                                                This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
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a 100 c
/mol_type="mRNA"
/db_xref="taxon:10090"
                                                                  rcy sequence stop: 408. Location/Qualifiers
                                  organism="Mus"
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   type="mRNA"

rref="+-
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/clone="IMAGE:318928" /dev_stage="19.5 dpc

dpc total fetus"

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JOURNAL
COMMENT
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AUTHORS
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AA499298
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ORGANISM
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                                                                                                                                                                                                                                                                               Unpublished
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutéleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 414)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T. Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              μ
                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                              4444 Forest Park I
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA499298
AA499298.1 GI:2232419
EST.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA499298
414 bp mRNA linear EST 01-JUL-1997
vh27e04.rl Soares mammary_gland_NbMMG Mus musculus cDNA clone
IMAGE.876702 5' similar to WP:ZK287.5 CE06614 ;, mRNA sequence.
                                                                                                                                                                                MGI:516182
                                                                                                                                                                                                                                                                                                                                                                                                          The WashU-HHMI Mouse EST Project
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                                                                                                                                                      primer: -28ml3 rev2 ET from Amersham
                                                                                                               quality sequence stop: 1
Location/Qualifiers
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1 others
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/mol_type="mRNA"
                                    /strain="C57BL/6J"
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/note="Vector: pT7T3D (Pharmacia) with a modified
/clone="IMAGE:876702"
                 db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH10B (ampicillin resistant)"
                                                                                                   .414
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Pred. No. 1.8e-55;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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                                                              source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                       CDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP CDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP CDNAs whose availability will be considered under appropriate and limited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BF469845 416 bp mRNA UI-M-BH3-atw-f-06-0-UI.rl NIH BMAP M S4 N UI-M-BH3-atw-f-06-0-UI 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                         8889548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 416)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                National Institute of Mental Health
                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF469845.1
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                                                                                                  collaborative arrangements
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                          20892-9643,
                                                                                                                                                                                                                                                                                                                             6001 Executive Blvd.
                                                                                                                                                                                                                                                                                                                                                                        Contact: Chin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGCTGC 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5'
organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bonaldo.
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/note="Organ: mammary_gland; Vector: pT7T3D-Pac (Pharmacia)
/note="Organ: mammary_gland; Vector: pT7T3D-Pac (Pharmacia)
/note="Organ: mammary_gland; Vector: pT7T3D-Pac (Pharmacia)
/note="Organ: mammary_gland" blanks; Site=1: Not I; Site=2: Eco
/note="Organ: mammary_gland" blanks; Site=1: Not I; Site=2: Eco
/note="Organ: mammary_gland" blanks; Site=1: Not I; Site=2: Eco
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/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                             ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                           Room 7N-7190, MSC 9643,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 127; DB 9;
Pred. No. 1.8e-55;
); Mismatches 0;
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BMAP_M_S4 Mus musculus cDNA clone
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; Murinae; Mus
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                   Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Ouackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S.
Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corban, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forres, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gisi, C., Godzik, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gisi, C., Godzik, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gisi, C., Godzik, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gisi, C., Godzik, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gisi, C., Godzik, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gisi, C., Godzik, G., Godzik, C., Godzik, G., Godzik, G., Godzik, G., God
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  into DH10B bacteria (LifeTechnologies) to generate the NIH BMAP M S4 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)"
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/lab_host="pH10B (Life Technologies)"
/clone_lib="NIH_BMAP M_S4"
/clone_lib="NIH_BMAP M_S4"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The Dolylinker; Site_1: Not I; sa subtracted library of a series, ultimateTy—derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain normalized libraries from ten regions of the mouse brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated
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Grimmond, S.,
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Gustincich, S.,
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Matches

BASE COUNT

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BY238589

RESULT 40

REFERENCE

AUTHORS

Hirokawa, N.,

Jackson, I.J.

Matches 127; Query Match Best Local Similarity

100.0%; ilarity 100.0%; Conservative 0.

0,

Score 127; DB 13; Pred. No. 1.8e-55; ; Mismatches 0;

Indels Length 418;

0;

Gaps

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DB 13;

SOURCE ORGANISM

**EYWORDS ERSION** 

FEATURES

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10). 1617-1620 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
,M., Miyata,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
,Sakazume,N., Sasaki,D., Saco,K., Shibata,K., Shiraki,T., Tagami
,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                      assistance we gratefully acknowledge. Please (http://genome.gsc.riken.go.jp) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIKEN 2-1 Hirosawa, Wako-shi, Saitama 351-0198 Japan ) whose assistance we gratefully acknowledge. Please visit our web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequencing pipeline with 384 multicapillary sequencer. 10 (11), 1757-1771 (2000)
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Tel: 81-45-503-9222
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Laboratory for Neuronal Circuit Development Brain Science Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Powan, W.J., Pertea, G., Decole G. Detrovsky, N. Billei B. Bonting, T. H. O. D.
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RIKEN integrated sequence analysis (RISA) system--384-format
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/tissue_type="visual cortex"
/clone_lib="RIKEN full-length enriched, visual cortex"
105 c     134 g     85 t
                                                                                                                                     /clone="K230007K04"
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                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                      location/Qualifiers
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427 bp mRNA linear EST 14-JUL-2000 us27h08.yl Soares NMEBA branchial arch Mus musculus cDNA clone IMAGE:3168351 5' similar to WP:R10A10.2 CE12670 ZINC FINGER PROTEIN
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NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
NRATIONAL CANCER INStitute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                   Seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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429 bp mRNA linear EST 11-SEP-2000 uw47g02.yl Soares mammary gland NMLMG Mus musculus cDNA clone IMAGE:3465170 5' similar to WP:R10A10.2 CE12670 ZINC FINGER PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contect: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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National Cancer Institute, Cancer Genome Anat
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                                                           CTGCTGC 213
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                                                                                                                                                                                   100.0%; !
ilarity 100.0%; !
Conservative 0;
                                                                                                                                                                                                                                                                      97
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                                                                                                                                                                                                                                                              /clone lib="Soares mammary gland_NMLMG"
/note="Vector: p?773D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p?773 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:3465170"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue_type="mammary gland"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                sex="female (lactating)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:10080085
                                                                                                                                                                                     Score 127; DB 10;
Pred. No. 1.8e-55;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Anatomy
                                                                                                                                                                                      Indels
                                                                                                                                                                                                                 Length 429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Project (CGAP),
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                                                                                                                                                                                     Gaps
                                                                                                                         185
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AUTHORS
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ORGANISM
                                                                                                                                                                                                                                                                                         BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Snoo
                                                                                                                                                                                                   Matches 127;
                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
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                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vp20a07.rl Soares mammary gland NbMMG Mus musculus cDNA IMAGE:1069140 5' similar to TR:P91404 P91404 SIMILARITY ZINC FINGER. ;, mRNA sequence.

AA815479
AA815479.1 GI:2885075
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The WashU-HMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4444 Forest Park |
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                  Similarity
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                                                                            CTGCTGC 127
                                                     primer: -28m13 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                         90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quality sequence stop: 3
Location/Qualifiers
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                                                                                                                                                                                                                                                                                         Bonaldo."
a 99 c
                                                                                                                                                                                                                                                                                                               adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                         primer (5'
                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares_mammary_gland_NbMMG"
/note="Organ: mammary_gland; Vector: pT7T3D-Pac (Pharmacia)
/ with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; 1st_strand_cDNA_was_primed_with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="IMAGE:1069140"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue_type="mammary gland"
dev_stage="4 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .440
                                                                                                                                                                                                                  100.0%;
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                                                                                                                                                                                                                Score 127; DB 9;
Pred. No. 1.9e-55;
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RESULT 44
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                                                                                                                                                                                             Matches
                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                               121
                                                               193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 314 200 1011
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA239898 443 bp mRNA linear mx81h04.rl Soares mouse NML Mus musculus cDNA clone similar to WP:ZK287.5 CE06614 ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waterston, R.
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1 (bases 1 to 443)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGI:426351
CIGCIGC
                               CTGCTGC 127
                                                             100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                quality sequence stop: .
Location/Qualifiers
                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="max....
/db_xref="taxon:10090"
/clone="IMAGE:692791"
/tissue_type="Liver"
                                                                                                                                                                                                                                                                      Bonaldo."
a 106 c
                                                                                                                                                                                                                                                                                                                                                             double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library
                                                                                                                                                                                                                                                                                                        constructed and normalized by
259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                  lib="Soares mouse NML"
                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                      144 g
                                                                                                                                                                                         Score 127; DB 9;
Pred. No. 1.9e-55;
; Mismatches 0;
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                                                                                                                                                                                                                                                                        93
                                                                                                                                                                                                                                                                                                      Bento Soares and M.Fatima
                                                                                                                                                                                                                         Length 443;
                                                                                                                                                                                           Indels
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IMAGE:692791 5'
                                                                                                                                                                                         0;
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121 CTGCTGC 127

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TITLE
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AUTHORS
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                                                                                                                      Query Match
Best Local Sim:
Matches 127;
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              28
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuc, Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
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W34374
W34374
MC56d06.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus clone IMAGE:352523 5' similar to WP:F35G12.9 CE00978 ;, mF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W34374.1 GI:1316302
EST.
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                                                                                                                                        Similarity
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                                                                               musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primer: ETPrimer
                                                                                                                                                                                                  104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               quality sequence stop: 444.
                                                                                                                      Conservative
                                                                                                                                                                                                               M.Fatima Bonaldo.
a 93 c 129 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="C57BL/6J"
/db_xref="taxon:10(
                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue_type="embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="IMAGE:352523"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                   dev_stage="13.5-14.5dpc total fetus"
lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex="unknown"
                                                                                                               100.0%; St.
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _xref="taxon:10090"
                                                                                                                    Score 127; DB 14;
Pred. No. 1.9e-55;
; Mismatches 0;
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AA036356
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MANUSCISCO 447 bp mRNA linear EST 26-AUG-1996 mi74f07.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:472357 5' similar to WP:F35G12.9 CE00978 ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Marra M/Mouse EST Project
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Location/Qualifiers
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//lab host="Mills (ampicillin resistant)"
//lab host="Phills (ampicillin resistant)"
//clone_lib="Soares mouse p3NMF19.5"
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RESULT 48
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450 bp mRNA linear EST 29-DEC-20 uz35e03.y1 NCI CGAP Mam5 Mus musculus cDNA clone IMAGE:3671068 5' similar to TR:Q9WTZI Q9WTZ1 ZINC RING FINGER PROTEIN SAG. ;, mRNA
sequence
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Seq primer: -40RP from Gibco
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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447 bp mRNA linear EST 27-SEP-2000 ux27909.y1 Soares NWMAX maxillary process Mus musculus cDNA clone IMAGE: 3511552 5' similar to TR:Q9WTZ1 Q9WTZ1 ZINC RING FINGER
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Location/Qualifiers
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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'db_xref="taxon:10090"
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Pred. No. 1.9e-55;
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Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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EST.
                                 Mus musculus
                                                   Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
.cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Washington University Genome Sequencing Cente
Clone distribution: NCI-CGAP clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                        215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="tumor, gross tissue"
/dev_stage="7 months" \
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/strain="C57BL/6J"
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Pred. No. 1.9e-55;
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Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                  visual cortex Mus musculus
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URL:http://genome.gsc.riken.go.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
                                                                                                                                                                                                                                                                                 Tissues were provided by Michela Fagiolini and Takao K. Hensch (Laboratory for Neuronal Circuit Development Brain Science Institute RIKEN 2-1 Hirosawa, Wako-shi, Saitama 35-0198 Japan ) whose assistance we gratefully acknowledge. Please visit our web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Re 10 (11), 1757-1771 (2000)
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
                                                                                                                                                                                                                                    assistance we gratefully acknowledge. Pleas
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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Best Local Similarity
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BY254133 RIKEN full-length enriched, v....
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schombach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Ouackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Geisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.B., Cosins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A.
                                                                                                                                                                  Nature 420,
22354683
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Okazaki, Y., Furuno, M.,
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                                                                                                          Contact: Yoshihide Hayashizaki
                                                                                                                                         12466851
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/clome="K330034814"
/tissue_type="visual cortex"
/clome_Tib="RIKEN full-length enriched, visual cortex"
/clome_Tib="RIKEN full-length enriched, visual cortex"
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Pred. No. 1.9e-55;
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prepare mouse tissues.

Presare mouse tissues.

Tissues were provided by Michela Fagiolini and Takao K. Hensch (
Laboratory for Neuronal Circuit Development Brain Science Institute
Laboratory for Neuronal Circuit Development Brain Science Institute
RIKEN 2-1 Hirosawa, Wako-shi, Saitama 351-0198 Japan ) whose
RIKEN 2-1 Hirosawa, Wako-shi, Saitama 351-0198 Japan ) whose
RIKEN 2-1 Hirosawa, Wako-shi, Saitama 351-0198 Japan ) whose
RIKEN 2-1 Hirosawa, Wako-shi, Saitama 351-0198 Japan ) whose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         assistance we gratefully acknowledge. Please visit o (http://genome.gsc.riken.go.jp) for further details.
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URL:http://genome.gsc.riken.go.jp/
URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
T., Timotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,
M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
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/mol type="mRNA"
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/clone_lib="RIKEN full-length enriched, visual cortex"
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Perfect score:
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                                      Unpublished

On Feb 15, 2001 this sequence version replaced gi:12881506.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 2013.f

more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI011AG11QP1&cluster=2013.f. Contact
Feng Liang Email : fliang@lifetech.com URL :
                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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                      TAAAAAAGAATGTTACAGTAACAAATAAAGTGCAGTTTAAA 754
                                                                     TATACAACAGGCAGTGGAAGCAGTTTC--GAGACTTTTTCGATGCTTATGGTTGATCAGT
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/clone_Tib="Homo sapiens PLACENTA COT 25 NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the PCMUSPORT 6 vector. Library was normalized
a 180 c 310 g 211 t 39 others
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/mol_type="mRNA"
/db_xref="taxon:9606"
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4e-183;
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Matches 739;
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
http://image.llnl.gov
http://image.llnl.gov
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BQ876591 853 bp mRNA linear AGENCOURT 8584244 Lupski_sympathetic_trunk Homo sandana:6192819 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BQ876591.1
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AATCATTCCTTCCACAACTGCTGCATGTCCCTGTGGGTGAAACAGAACAATCGCTGCCCT
                                                               TGTCTTAGATGTCAAGCTGAAAACAAACAAGAGGACTGTGTTGTGGTCTGGGGAGAATGT
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Location/Qualifiers
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1 kb for average insert length 1.9 kb. This is a primary
library, non-amplified Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylo
College of Medicine); available through Life
Technologies."

191 c 225 g 205 t 1 others
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/dev_stage="adult, 16 yr"
/lab_host="DH10B",
/clone_lib="Lupski_sympathetic_trunk"
/clone_lib="Lupski_sympathetic_trunk"
/note="Vector: pCMV-SPORT6 (Life Technologies);
NotI; Site_2: Sall; cDNA made by oligo-dT primin
Directionally cloned using the following adaptor
5'-TCGACCCACGCGTCCG-3' and
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/mol_type="mRNA"
/db_xref="taxon:9606"
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97.1%;
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Pred. No. 1.1e-181;
0; Mismatches 15;
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                                                                                                                                                  Contact: Genoscope
Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
Email: segvef@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2013.f For
more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0A1037CH07Qp1
&cluster=2013.f. Contact: Feng Liang Email: fliang@lifetech.com
URL: http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0AI037CH07Qp1.
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BX324742.1
EST.
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Mammalia; Eutheria; Primates;
1 (bases 1 to 1201)
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BX324742 Homo sapiens PLACENTA COT 25-NORM
clone CSODIO37YP13 5-PRIME, mRNA sequence.
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     /tissue_type="placenta cot 25-NORMALIZED"
/clone_lib="Homo sapiens placenta COT 25-NORMALIZED"
/note="let strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                     organism="Homo
                                                                                 clone="CS0DI037YP13"
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Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata;
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602743362F1 NIH_MGC_49 Homo
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RESULT 3 BX324742 LOCUS

DEFINITION

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ACCESSION VERSION KEYWORDS

REFERENCE AUTHORS TITLE

COMMENT

JOURNAL

FEATURES

Vertebrata;

Euteleostomi;

clone

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655 680 536

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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1750 row: k column: 16
High quality sequence stop: 748.
Location/Qualifiers
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National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Primates; Catarrhini; 1 (bases 1 to 949)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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                                                                                    TTCAGAGCCCTGGTGGATCTTGTAATCCAGTGCCCTACAAGGCTAGAACACTACAGGGG
                                                                                                                                                          GACTGGGTGGTCCAAAGAATCGGCAAATGAGAGTGGTTAGAAGGCTTCTTAGCGCAGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage_resistant)"
/clone_lib="MIH_MCC_49"
/clone_lib="MIH_MCC_49"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor:
GCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Library.
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cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The L.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
plate: LLAMI1556 row: i column: 06
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1 (bases 1 to 797).
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg,
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                                                                                                                208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       quality sequence stop:
Location/Qualifiers
                                                                                                         /note="forgan: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."

a 179 c 212 g 198 t
                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5221325"
                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
|mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                      lab_host="DH10B"
                     87.7%;
                                                                                                                                                                                                                                                                                                                                              _lib="NIH_MGC_120"
Score 661.6; DB 12;
Pred. No. 1.8e-175;
0; Mismatches 14;
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ATGGCCGACGTGGAAGACGGAGAGGAAACCTGCGCCCTGGCCTCTCACTCCGGGAGCTCA

Matches 740;

Conservative

0;

Indels

10;

Gaps

6

60

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REFERENCE
AUTHORS
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ORGANISM
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                      mRNA sequence.
BI759082
                                                                                                                                                                                                                                                      918
603042879F1 NIH_MGC_116 Homo
mRNA sequence
                                                                                                                                                                                                                        BI759082.1 GI:15750660
                                                                                Unpublished
                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11457 row: m column: 20
High quality sequence stop: 732.
Location/Qualifiers
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                                                ATCAAAGCCTTGGTT--AGCATTTGTCAGTTTTATCTTCAGAAATTCTCTGTGAGTTAAGA
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                                ATCAAAGCCTTGGTTTAGCATTTTGTCAGTTTTATCTTCAGAAATTCTCTGCGATTAAGA
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//clone_lib="NIH MGC 116"
//clone="Ozgan: pooled colon, kidney, stomach; Vector:
//core="Ozgan: pooled colon, kidney, stomach; Vector:
pCMV-SPORTG; Site_1: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH MGC Library."
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/mol type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5183419"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.5%;
96.7%;
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JOURNAL
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Contact: Robert Strausberg, Ph.D.
Email: ggapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shira
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1701 row: g column: 04
High quality sequence stop: 780.
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1 (bases 1 to 818)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished
                                                                                                                                                                                                                                                                           Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
BI457840
                                                                                                                                                                                                                                                                                                                                                               818 bp mRNA line
603198212F1 NIH MGC_96 Homo sapiens cDNA clone
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TATACAAACAGGCAGTGGAAGCAGTTTCAGAGAACTTTTTTGCATTGCTTATGGTTGATC
              TATAC-AACAGGCAGTGGAAGCAGTTTC----GAGACTTTTTCGATGCTTATGGTTGATC
                                                                                      AGATAATTTATTAAAGGTGGTCCTTCCTACCTCTGTGGTGTGTCGCGCACACAGCTTA
                                                                                                         ATCAAAGCCTTGGTTTAGCATTTTGTCAGTTTTATCTTCAGAAATTCTCTGCGATTAAGA
                                                                                                                                                                               ACACTACAGGGGATGAATTCTTCAAATAGGAGCCGATGGATCTGTGGTCCTTTGGGACTC
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/db_xref="taxon:9606"
/clone="IMAGE:5277723"
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95.6%;
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Sh

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 805)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
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  TGTCTTAGATGTCAAGCTGAAAACAAACAAGAGGACTGTGTTGTGGTCTGGGGAGAATGT
                          TGTCTTAGATGTCAAGCTGAAAACAAACAAGAGGACTGTGTTGTGGTCTGGGGGAGAATGT
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="NIH_MGC_96"
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTTTVN-3', size-selected for average insert size_2: Xb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

a 183 c 214 g 194 t
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4793091"
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/lab_host="DH10B"
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94.6%;
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Pred. No. 1.3e-170;
0; Mismatches 31;
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                                                                                    Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: WGC clone distribution-information car
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1725 row: j column: 07
High quality sequence stop: 820.
Location/Qualifiers
                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits,
cDNA Library Preparation: Michael J.
                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 856)
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603244729F1 NIH_MGC_96 Homo sap
                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
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/clone="MAGE:5287014"
/tissue_type="hypothalamus"
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                                                                        TCTATACAACAGGCAGTGGAAGCAGTTTC--GAGACTTTTTCGATGCTTATGG--TTGAT
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CAGTTAAAAAAGAATGTTACAGTAACAAATAAAGTGCAGTTTAAA 754
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                                          TCTATACAACAGGCAGTGGAAGCAGTTTCAGAGAACTTTTTGCATGCTTATGGGTTGATC
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EST.
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1743 row: e column: 04
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National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 754)
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                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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GACTGGGTGGTCCAAAGAATCGGCAAATGAGAGTGGTTAGAAGGCTTCTTAGCGCAGTTG
                               GACTGGGTGGTCCAAAGAATCGGCAAATGAGAGTGGTTAGAAGGCTTCTTAGCGCAGTTG
                                                                                             CACAACTGCTGCATGTCCCTGTGGGTGAAACAGAACAATCGCTGCCCTCTCTGCCAGCAG
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/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC 49"
/clone lib="NIH MGC 49"
/note="organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
/note="organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
/ECORI; CDNA made by oligo-dT priming. DIrectionally cloned into EcoRI/XhoI sites using the following 5: adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC
Library. | "
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'db_xref="taxon:9606"
'clone="IMAGE:4870251"
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Plate: LLAM12748 row:
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Tissue Procurement: ATCC
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National Institutes of Health,
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:5737890"
/tissue_type="duodenal adenocarcinoma, cell line"
/tosue_type="duodenal adenocarcinoma, cell line"
/tosue_type="duodena
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BM704660 706 bp mRNA linear EST 28-
UI-E-CI1-afo-o-15-0-UI.r2 UI-E-CI1 Homo sapiens cDNA clone
UI-E-CI1-afo-o-15-0-UI 5', mRNA sequence.
BM704660
1 (bases 1 to 706)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two appr
                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                            Homo sapiens
                                                                                                                                   Homo sapiens (human)
                                                                                                                                                                            BM704660.1 GI:19017918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Res. 6 (9), 791-806
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Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Soares, MB
Coordinated Laboratory
University of Iowa
375 Newton Road , 4156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetics (www.resgen.com).
Seq primer: M13 Reverse.
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//mol type="mRMA"
//db_xref="taxon:9606"
//clone="UI-E-CII-afo-o-15-0-UI"
//tissue type="mRPE and Choroid"
//tissue type="mRPE and Choroid"
//dev_stage="adult"
//dev_stage="adult"
//lone_lib="UI-E-CII"
//clone_lib="UI-E-CII"
//note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-E-CII is a normalized CDNA library containing the following tissue(s): RPE and Choroid. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I; and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute
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Pred. No. 8.3e-168;
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В

REFERENCE AUTHORS TITLE

364

VERSION KEYWORDS SOURCE

ORGANISM

ACCESSION DEFINITION

RESULT 13 BM704660 LOCUS

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772 709

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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BI226556
602951527F1 NIH_MGC_8 Homo
mRNA sequence.
BI226556
BI226556.1 GI:14680000
                                                                                                                                                                                                                                                                                                                                                                               Plate: LLCM1866 row: f column:
High quality sequence stop: 720.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 724)
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National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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                      195
             /clone="IMAGE:5095687"
/tlssue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_8"
/clone_lib="NIH_MGC_8"
/clone_lib="NIH_MGC_8"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI, CIDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
95 a 153 c 189 g 187 t
                                                                                                                                                                                                                                                                                                   db xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
|mol_type="mRNA"
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no sapiens
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Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; I

Mammalia; Eutheria; Primates; Catarrhini; Hominidae;

1 (bases 1 to 922)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collect
                                                                                                                 AGENCOURT 7968580 NIH MGC 68
5', mRNA sequence.
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
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Plate: LLAM13200 row: h column: 20
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                                                                                                                      ATCAAAGCCTTGGTT--AGCAITTGTCAGTTTTAICTTCAGAAATTCTCTGTGATTAAGA
GAAGTGCTATAAAAAAGGAAAGAGCTCCAAATTGAATCACC-TTATAATTTACCCATTTC
                                                               ATCAAAGCCTTGGTTTAGCATTTTGTCAGTTTTATCTTCAGAAATTCTCTGCGATTAAGA
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                                 AGATAATTTATTANAGGTGGTCCTTCCTACCTCTGTGGTGTGTGTCGCGCACACAGCTTA
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/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_68"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo (
Average insert size 1.8 kb. Library constructed by Li
Technologies. "
202 c 250 g 220 t 1 others
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/db_xref="taxon:9606"
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NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Location/Qualifiers
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Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished Contact: Robert Strausberg, Ph.D.
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/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_9"
/clone_lib="NIH_MGC_9"
/cloned_lib="NIH_MGC_9"
/cloned_into_vary; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2: /cloned_into_branched_lib="Core interestants"
/cloned_into_branched_by_oligo-dT_priming. Directionally cloned_into_branched_by_oligo-dress_into_folionally cloned_into_branched_by_oligo-dress_into_folionally cloned_into_folionally cloned_into_fol
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/db_xref="taxon:9606"
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                                                                                                  Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Sh
Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

cDNA Sequencing by: Incytte Genomics, Inc.

Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10038 row: d column: 04

High quality sequence stop: 741.
                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence. — — BG037017
BG037017.1 GI:12432822
EST.
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                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4374483"
/tissue_type="hypothalamus"
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ACCESSION

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                                                                            AGAAGTGCTATAAAAAAAGGAAAGAGCTCCAAATTGAATCACC-TTATAATTTACCCATTT
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/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhOI (gtcg pBluescript KS+); Site_1 BamHI; Site_2: SalI-XhOI (gtcg pBluescript KS+); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3' size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched
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cgi-bin/cluster-cgi?seq=CSOA1037CH07NP1&cluster=2013.f. Contaged Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOA1037CH07NP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 2013.f, For more information, about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                    ACACTACAGGGGATGAATTCTTCAAATAGGAGCCGATGGATCTGTGGTC--TTTGGACTC 478
ANACTACAGGGGATGAATTCTTCAAATAGGAGCCGATGGATCTGTGGTCCTTTGGNANTC
                                                                                                       TTAGCGCAGTTGTTCAGAGCCCTGGTGGATCTTGTAATCCAGTGCCCTACAAAGGCTAGA
                                                                                                                                                    NTCTGCCAGCAGGACTGGGTCCAAAGAATCGGCAAATGANAGTGGTTAGAAGGCTTC
                                                                                                                                                                                           CTCTGCCAGCAGGACTGGGTGGTCCAAAGAATCGGCAAATGAGAGTGGTTAGAAGGCTTC
                                                                                                                                                                                                                                  AATNATTCCTTCNACAACTGCTGCATGTCCCTGTGGGTGANACAGGANAATNGCTGCCCT
                                                                                                                                                                                                                                                                           AATCATTCCTTCCACAACTGCTGCATGTCCCTGTGGGTGAAACAGAACAATCGCTGCCCT
                                                                                                                                                                                                                                                                                                                                       TGTCTTAGATGTCAAGCTGAAAAACAAACAAGAGGACTGTGTTGTGGTCTGGGGAGAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                      GGCTCCAAGTCGGGAGGCRACAAGATGTTCTCCCTCAAGAAGTGGAACGCGGTGGCCATG
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/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Let strand cDNA was primed with a NotI-oligo(dT)
primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
a 249 c 234 g 299 t 136 others
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/db_xref="taxon:9606"
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Pred. No. 1.8e
6; Mismatches
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1.8e-163;
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Best Local S
Matches 725
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                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution i found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                             Plate: LLAM12001 row: o column: High quality sequence stop: 718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria;
1 (bases 1 to 797)
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                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                GCCGACGTGGAAGACGGAGAGGAAACCTGCGCCCTGGCCTCTCACTCCGGGAGCTCAGGC
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                                                                                                                                           /note="Organ: breast; Vector: pcMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; Oligo-dT primed. Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                     /clone="IMAGE:5393131"
/tissue_type="mammary adenocarcinoma,
/lab_host="pH10B (phage-resistant)"
/clone_lib="NIH_MGC_87"
                                                                                                                                                                                                                                                                                                                                             /mol
                                                                                                                                                                                                                                                                                                                           db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
|mol_type="mRNA"
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95.0%;
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Pred. No. 1.:
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KEYWORDS
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AGENCOURT 8298360 NIH_MGC_100 Homo sapiens
5', mRNA sequence.
BQ648608
BQ648608.1 GI:21772780
EST.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                   1 (bases 1 to 983)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_100"
/clone_rib="NIH_MGC_100"
/note="forgan: liver; vector: pOTB7; Site_1: XhoI; Site_2:
/note=-forgan: liver;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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National Institutes of Health, Mammalian Gene Collection (MGC)
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TGTCTTAGATGTCAAGCTGAAAACAAACAAGAGGACTGTGTTGTGGTCTGGGGAGAATGT
                                                                                                    GGCTCCAAGTCGGGAGGCGACAAGATGTTCTCCCTCAAGAAGTGGAACGCGGTGGCCATG
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//Clone="IMAGE:4875489"
//Lissue_type="normal pigmented retinal epithelium"
//Lab_host="DH10B (phage-resistant)"
//Clone_lib="NIH_MGC_43"
//note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CNNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. | "
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/mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                         Score 609; DB 10;
Pred. No. 1.3e-160;
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                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NF
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
cDNA Library Arrayed by: The I.M.A.G.E.
                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homc (bases 1 to 767)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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BI601470
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                                                                                                                                                                       found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5300845"
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  ACGTTTAAAA
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/lab_host="DH10B"
/clone_lib="NIH_MGC_96"
/clone_lib="NIH_MGC_96"
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/clone_lib="NIH_MGC_96"
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/clone_lib="NIH_MGC_96"
/clone_lib="NIH_MGC_96"
/clone="Normalication brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag pBluescript KS+); Site_1: SalI-XhoI (gtcgag pBluescript TTTTTTTTVN-3', size_selected for average insert 5:ze_2: Ab and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 702)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insert Length: 854 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality serveror
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Email: Cappbs-Femail.nih.gov

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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Location/Qualifiers
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//lab_host="DH10B"

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1939252"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Sh
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 847)
1 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
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602720212F1 NIH MGC 97 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLAM10769 row: g column: 03 High quality sequence stop: 775.

Location/Qualifiers
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//clone | lib="NHH MCC 97"

//clone | lib-mack 97"

//clone | lib-mac
                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4837274"
/lab_host="DH108"
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3 CDNA clone IMAGE:4837274 5',
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10578 row: e column: 23
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Tissue Procurement: DCTD/DTP
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                      CACACAGCTTAGAAGTGCTATAAAA-AAGGAAAGAGCTCCAAATTGAATCACC-TTATAA
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/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH108 (phage-resistant)"
/clone_lib="NIH_MGC 87"
/clone_lib="NIH_MGC 87"
/note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution informatifound through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

DAM385 row: b column: 14
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1 (bases 1 to 782)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
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Tissue Procurement: Dr. Stefan Hansson
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                   ATGGCCGACGTGGAAGACGGAGAGGGAAACCTGCGCCCTGGCCTCTCACTCCGGGAGCTCA 60
                         GGCTCCAAGTCGGGAGGCGACAAGATGTTCTCCCTCAAGAAGTGGAACGCGGTGGCCATG
                                                                                                                                                           ATGGCCGACGTGGAAGACGGAGAGGAAACCTGCGCCTGGCCTCTCACTCCGGGAGCTCA
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TGGTTGATCAGTTAAAACCGAATGTTACAGTAACAAATACAGTGCAGTTTAAA
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                                                                                                                                                                                                                                                                                                                                              195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e: NDAM385 row: b column: quality sequence stop: 635. Location/Qualifiers
                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                        /clone lib=NIH MGC_147"
/clone lib=NIH MGC_147"
/note="Organ: placenta; Vector: pBluescriptR; Site_1:
/note="Organ: placenta; Vector: pBluescriptR; Site_1:
/note="Organ: placenta; Oligo-dT primed using primer sl1-xho1; Site_2: BanH; Oligo-dT primed using primer size e.3. kb and normalized to ROT 5: This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: This is a NIH MGC library."
95 a 186 c 215 g 186 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Human Placenta"
/lab_host="DH10B TonA"
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                                                                                                                                                                                                                                                             96.6%;
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                                                                                                                                                                                                                                                           Score 603.4; DB 14; Pred. No. 4.9e-159;
                                                                                                                                                                                                                                          Mismatches
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mRNA sequence.
BG742338
BG742338.1 GI:
EST.
                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arayed by: The I.M.A.G.E. Consortium (LLN
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM10630 row: m column: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Butheria; Primates; Catarrhini;
1 (bases 1 to 904)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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602631707F1 NCI_CGAP_Skn3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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                                                                                                                                                                                                      quality sequence stop: 836.
Location/Qualifiers
/mol_type="mRNA"
/db xref="taxon:9606"
/db yref="taxon:97129"
/clone="IMAGE:4777129"
/lab host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Skn3"
                                                                                                                                             organism="Homo sapiens"
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                                                  CA449255 mRNA 1
UI-H-ED0-ays-n-12-0-UI.s1 NCI CGAP_ED0 Homo
UI-H-ED0-ays-n-12-0-UI 3', mRNA sequence.
CA449255
CA449255.1 GI:24813675
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Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@ulowa.edu
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Mammalia; Eutheria;
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//note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
//note="Organ: Left Pubic Bone; Vector: Leon Research, Genome Research, Genome
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/tlssue_type="Chondrosarcoma"
/dev_stage="Adult"
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1 (Dases 1 to 716)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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BG761806
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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                                    /tissue_type="melanotic melanoma, high MDR (cell line)"
/lab host="DHIOB (phage resistant)"
/clone libs"NIH MCC 49"
/clone libs"NIH MCC 49"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GCCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
ILRT (Life Technologies). Note: this is a NIH_MGC
using ZAP-CHNA SYMPHOLOGIES). Note: this is II RT (Life Technologies). Note: this is Library. |"
                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Best Local Similarity
Matches 664; Conser
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                    Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 840)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections
             Unpublished
                                                                                       Homo sapiens
                                                                                                                EST
                                                                                                                            BG037022
BG037022.1 GI:12432833
                                                                                                                                                 mRNA sequence
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GATAATTTA-TTAAAGGTGGTCCTTCCTACCTCTGTGGTGTGTGTCGCGCACACAGC-TT
                                      ATCAAAGCCTTGG-TTAGCATTTGTCAGTTTTATCTTCAGAAATTCTCTGTGATTAAGAA
                                                                         ACACTACAGTGGATGAATTCTTCAAATAGGAGCCGATGGATCTGTGGTCCTTTGGGACTC
                                                                                          ACACTACAGGGGATGAATTCTTCAAATAGGAGCCGATGGATCTGTGGTC--TTTGGACTC
                                                                                                                                                                                                                                              AATCATTCCTTCCACAACTGCTGCATGTCCCTGTGGGTGAAACAGAACAATCGCTGCCCT
                      ATCAAAGCCTTGGTTTAGCATTTGTCAGTTTTATCTTCAGAAATTCTCTGCGATTAAGAA
                                                                                                                                           TTAGCGCAGTTGTTCAGAGCCCCTGGTGGATCTTGTAATCCAGTGCCCTACAAAGGCTAGA
                                                                                                                                                                         CTCTGCCAGCAGGACTGGGTGGTCCAAAGAATCGGCAAATGAGAGTGGTTAGAAGGCTTC
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Location/Qualifiers
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92.7%;
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568

508 478 448 420 360

388

300

268

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DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM10038 row: b column: 12 High quality sequence stop: 806.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Libarary Preparation: Michael J. Brownstein
Toshiyuki and Piero Carninci (RIKEN)
cDNA Libarary Arrayed by: The I.M.A.G.E. Consorti
TGTCTTAGATGTCAAGCTGAAAACAAACAAGAGGACTGTGTTGTGGTCTGGGGAGAAATGT
                                                                         GGCTCCAAGTCGGGAGGCGACAAGATGTTCTCCCTCAAGAAGTGGAACGCGGTGGCCATG
                                                                                                                                                    GGCTCCAAGTCGGGAGGCGACAAGATGTTCTCCCTCAAGAAGTGGAACGCGGTGGCCATG 120
                                                                                                                                                                                                                                        ATGGCCGACGTGGAAGACGGAGAGGAAACCTGCGCCCTGGCCTCTCACTCCGGGAGCTCA
                                                 ATGGCCGACGTGGAAGACGGAGAGGAAACCTGCGCCCTGGCCTCTCACTCCGGGAGCTCA
                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="hypothalamus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4374443"
                                                                                                                                                                                                                                                                             Score 592.8; DB
Pred. No. 5e-156;
0; Mismatches 4
                                                                                                                                                                                                                                                                               42;
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BASE COUNT
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AUTHORS
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                                                                                  Query Match
Best Local Similarity
Matches 653; Conser
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JOURNAL
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    13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11414 row: h column: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BI828930.1 GI:15940480
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1 (bases 1 to 827)
                                ATGGCCGACGTGGAAGACGGAGAGGAAACCTGCGCCCTGGCCTCTCACTCCGGGAGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCCAGTTAACAAAGAAGTGTCCGTACACAATAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quality sequence start: 2 quality sequence stop: 679. Location/Qualifiers
                                                                                                                                                                                /clone lib="NIH MGC 119"
/clone lib="NIH MGC 119"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Cross organ: vector organ: ve
                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="medulla"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/clone="IMAGE:5166790"
                                                                                                       78.2%;
97.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  type="mRNA"
                                                                                  Score 589.6; DB Pred. No. 4e-155; 0; Mismatches
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                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
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                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                     Unpublished
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FEATURES
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12007 row: m column: 21
High quality sequence stop: 675.
Location/Qualifiers
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/lab host="DH10B (phage resistant)"
/clone_lib="NIH_MGC_87"
/clone_lib="NIH_MGC_87"
/note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Sterage insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC_Library."
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/db_xref="taxon:9606"
/clone="IMAGE:5395388"
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10033 row: n column: 20
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BG111792.1 GI:12605298
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Tissue Procurement: ATCC
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/db xref="taxon:9606"
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/tissue_type="osteosarcoma, cell line"
/tissue_type="osteosarcoma, cell line"
/tlab host="DHIOB (phage-resistant)"
/clone_lib="NIH_MGC_86"
/clone=[lib="NIH_MGC_86"
/note="Organ: bone; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: bone; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.533 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

Note: this is a NIH_MGC Library."

1 others
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Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scaarce,M., Brestalli,J., Gradwohl,G., Clitton,S., Hillier,L., Marra,M., Pape,D., Wylle,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,B., Ronko,I., Bennett,J., Cardenas ,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing
Washington University Genome Sequencing Center For informat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence.
BQ632594
BQ632594.1 GI:21684112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                obtaining a clone please contact:
(hinoue@im.wustl.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 617-495-1812
Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Other_ESTs: i125c04.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi
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1 (bases 1 to 629)
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    Gibbons, M., McCann, R., Cole, R.,
Jackson, Y. and Bowers, Y.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       quality sequence stop:
Location/Qualifiers
                               /note="Organ: Pancreas; Vector: pBluescript SK(-); Site 1:
NotI; Site 2: XhoI, cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab); Mashington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                          /lab_host="DH10B"
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/tissue_type="Purified pancreatic islet"
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REFERENCE AUTHORS

iomo sapiens

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 745)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE

COMMENT

Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, CDNA Library Arrayed by: The I.M.A.G.E. Cons DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution i

Consortium

Contact: Robert Strausberg, Ph.D.

Unpublished

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KEYWORDS
SOURCE
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                   AACAGGCAGTGGAAGCAGTTTCGAGACTTTTTCGATGCTTATGGTTGATCAGTTAAAAAA
                                                                                                                                                                                  CAAAGCCTTGGTTAGCATTTGTCAGTTTTATCTTCAGAAATTCTCTGTGATTAAGAAGAT
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/mol type="mRNA"
/mb_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:4449693"
/tissue_type="adenocarcinoma, cell line"
/lab host="PH10B (phage-resistant)"
/clone lib="MIH MGC 90"
/clone lib="MIH MGC 90"
/site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
96 a 157 c 209 g 183 t
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93.5%;
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Pred. No. 4.1e-
0; Mismatches
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-GGATGCTATGGTTGATCAGGTAAGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium ()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Home 1 (bases 1 to 734)
NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 667
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE397308.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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Clone distribution: MGC clone distribution information can
GTGAAACAGAACAATCGCTGCCCTCTCTCTGCCAGCAGGACTGGGTCGAAAGAATCGGC
                                                                                                                                                                                                                                                                                                                                                                    AAGAAGTGGAACGCGGTGGCCATGTGGAGCTGGGACGTGGAGTGCGATACGTGCGCCATC
                                                                                                                                  TGTGTTGTGGGTCTGGGGAGAATGTAATCATTCCTTCCACAACTGCTGCATGTCCCTGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE::619424"
/tissue_type="Burkitt lymphoma"
/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_8"
/clone="Organ: lymph; vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: lymph; vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: lymph; vector: pOTB7; Site_1: XhoI; Site_2:
/cloned into EcoRI/XhoI sites using the following 5:
/cloned into EcoRI/XhoI s
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 6e-153;
0; Mismatches 3
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Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
BI757881
BI757881.1 GI:15749459
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603030486F1_NIH_MGC_114
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                          Plate: LLAM11502 row: 1 column: High quality sequence stop: 667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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/clone_lib="NIH_MGC_114"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: policy organ: pCMV-SPORT6; Site_1: Not1;
/note="Organ: pCMV-SPORT6; Site_1: Not1;
/not
                                                                                                                                                                                                                 /mol_type= "max."
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                           organism="Homo sapiens"
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                                                                                                                                                                                                          clone="IMAGE:5200676"
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Local Similarity
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                         TTGATCAGTTAAAAAAGAATGTTACAGTAACAAATAAAGTGCAGTT
                                                                                                      CATTTCTATACAACAGGCAGT-GGAAGCAGTTTC----GAGACTTTTTCGATGCTTATGG
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Metazoa; Chordata; Craniata; Vertebrata;

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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shira
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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1 (bases 1.to 793)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
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/clone lib=WIH MGC 96"
/note="Organ: brain; Vector: pBluescriptR (modified /note="Organ: brain; Vector: pBluescriptR (site 2: SalI-XhoI (gtcgag pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag pBluescript KS+); Site 2: SalI (gtcgag pBluescript KS+);
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/tissue_type="hypothalamus"
/lab_host="DH10B"
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Query Match Best Local Matches 61	BASE COUNT	FEATURES SOURCE	RESULT 39 BG71465 LOCUS LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9
Query Match 75.8%; Score 571.8; DB 10; Length 651; Best Local Similarity 98.1%; Pred. No. 3.8e-150; Matches 611; Conservative 0; Mismatches 7; Indels 5; Gaps 3;	/organism="Homo sapiens" /mol type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:4799834" /tissue_type="hypothalamus" /lab host="DH10B" /lab host="DH10B" /clone_lib="NIH_MGC_96" /note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."  157 a 148 c 190 g 156 t	Tissue Procurement: Mikla CDNA Library Preparation CDNA Library Preparation Toshiyuki and Piero Carn. CDNA Library Arrayed by Incyl NA Sequencing by: Incyl Clone distribution: MGC found through the I.M.A. ohttp://image.llnl.gov plate: LLAMI0689 row: o High quality sequence sto Location/Qualification (Clone Sto Location)	BG714665  BG714665  MRNA Sequence.  BG714665.1 GI:13993596  BG714665.1 GI:13993596  BG714665.1 GI:13993596  BG714665.1 GI:13993596  SGT.  HOmo sapiens (human)  Homo sapiens Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  Eukaryota; Metazoa; Chordata; Craniata; Hominidae; Homo.  1 (bases 1 to 651)  1 (bases 1 to 651)  National Institutes of Health, Mammalian Gene Collection (MGC)  Unpublished  Contact: Robert Strausberg, Ph.D.  Email: Capabs-remail nith Gov	479 ATCAAAGCCTTGGTTAGCATTTGTCAGTTTTATCTTCAGAAATTCTCTGTGATTAAGA 536

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ATGGCCGACGTGGAAGACGGAGAGGAAACCTGCGCCCTGGCCTCTCACTCCGGGAGCTCA

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MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biol
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BQ632301.1
                                      Contact: Douglas Melton, Klaus H. Kaestner
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical
Dept of Molecular and Cellular Biology, 7
                                  Dept of N
MA 02138
                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 641)

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenac,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,J., Jackson,Y. and Bowers,Y.
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641 bp mRNA linear EST 02-JUL-2002 il25c04.xl HR85 islet Homo sapiens cDNA clone IMAGE:6031086 3' similar to TR:Q9Y5M7 Q9Y5M7 RING FINGER PROTEIN. [1] ;, mRNA
                                                                                                       Endocrine Pancreas Consortium
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dmelton@biohp.harvard.edu
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Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40UP from Gibco
High quality sequence stop: 449.
Location/Qualifiers
AAAAGAATGTTACAGTAACAAATAAAGTGCAGTTTAAA
                                                                                                            ACAACAGGCAGTGGAAGCAGTTTCGAG--ACTTTTTCGATGCTTATGGTTGATCAGTTAA
                                                                                                                                                                                                       GTGCTATAAAAAAGGAAAGAGCTCCAAATTGAATCACC-TTATAATTTACCCATTTCTAT
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//Clone_lib="HR85 islet"
//note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
76 a 159 c 125 g 181 t
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="Purified pancreatic islet"
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Pred. No. 1.3e-148;
0; Mismatches 11;
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Best Local Similarity
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Plate: LLCM2672 row: c column:
High quality sequence stop: 527.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: NCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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AGENCOURT 10018944 NIH MGC 142 Homo
IMAGE: 6495009 5', mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                        ATGTCAAGCTGAAAACAAACAAGAGGACTGTGTTGTGGTCTGGGGAGAATGTAATCATTC
                                                                                                                                                             CTTCCACAACTGCTGCATGTCCCTGTGGGTGAAACAGAACAATCGCTGCCCTCTCTGCCA
                      CTTCCACAACTGCTGCATGTCCCTGTGGGTGAAACAGAACAATCGCTGCCCTCTCTGCCA
                                                                   ATGTCAAGCTGAAAACAAGAGAGGACTGTGTTGTGGTCTGGGGAGAATGTAATCATTC 120
                                                                                                                                         AAAAGAATGTTACAGTAACAAATAAAGTGCAGTTTAAA
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                                                                                                                                                                                                                                                                                                     185
                                                                                                                                                                                                                                                                                        /tissue type="mixed (pool of 40 RNAs)"
/lab host="DH10B (T1-phage-resistant)"
/clome lib="NIH_MGC_142"
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
Site 2: SfiI (ggccgctcggcc); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
4%; connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%,
ovary - 4%, pharynx - 2.5%, prostate - 4.3%, sallvary
gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were
sed in cloning as follows:
-ANGCAGTGGTATCAACGCAAGAGTGGCCATTACGGCCGGG-3' and
5'-ANTCTAGAGGCCGAGCGAGCAAGTGT(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the >0.5 kb
size fraction (other fractions present in NIH MGC 141).
Library created in the laboratory of M. Brownstein (NIMH,
Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
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'clone="IMAGE:6495009"
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CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM468 row: h column: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 946)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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AGENCOURT 14477072 NIH MGC 179 Homo
IMAGE:30392712 5', mRNA sequence
CD556579
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                  quality sequence start: 22 quality sequence stop: 606 Location/Qualifiers
/clone="IMAGE:30392712"
/tissue_type="Pituitary"
/lab_host="DH10B-Ton A ( T1
                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                 organism="Homo
                                                                                                                                 sapiens,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/note="Organ: brain; Vector: pCMV-SPORT6.1; Site_1: EcoRV (destroyed); Site_2: Mot1; Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.1 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC Library."

[1] A SPORT SITE STATE S
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Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation:
cDNA Library Preparation:
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
Plate: LLNM12898 row: M. column: 19
Plate: LLNM12898 row: M. column: 19
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1 (bases 1 to 622)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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                          ACACTACAGGGGATGAATTCTTCAAATAGGAGCCGATGGATCTGTGGTC--TTTGGACTC
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Normalized to Cot5. Primary library, non-amplified.
Library constructed by M. Lovett. For more information of this library, please contact R. Tidwell (Washington University) or visit the COGENE website at http://hg.wustl.edu/COGENE/."

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/db_xref="taxon:9606"
/clone="IMAGE:5795514"
/tissue_type="mandible, pooled"
/dev_stage="embryo, 6 weeks postconception"
/lab_host="DH10B"
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UI-E-CI1-afo-o-15-0-UI.sl UI-E-CI1 Homo sapiens cDNA clone
UI-E-CI1-afo-o-15-0-UI 3', mRNA sequence.
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
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BU730720.1 GI:23654893
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
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Seq primer: M13 FORWARD
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/mol type="mRNA"
/db_xref="taxon:9606"
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/clone="UI-E-C11-afo-o-15-0-UI"
/tissue_type="RPE and Choroid"
/dev_stage="adult"
/lab_host="PH108 (Life Technologies) (TI phage resistant)"
/lab_host="PH108 (Life Technologies) (TI phage resistant)"
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1 (bases 1 to 595)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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                                                                                                         Contact: Robert Strausberg, Ph.D
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BG026092 781 bp mRNA linear EST 24-J7 60229288F1 NIH MGC 86 Homo sapiens cDNA clone IMAGE:4387076 mRNA sequence.
BG026092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                      TGGTTAGAAGGCTTCTTAGCGCAGTTGTTCAGAGCCCTGGTGGATCTTGTAATCCAGTGC
                                                                                                       TCGCGCACACAGCTTAGAAGTGCTATAAAAAAAGGAAAGAGCTCCAAATTGAATCA
                                                                                                                                                                                                   GGTC--TTTGGACTCATCAAAGCCTTGGTT----AGCATTTGTCAGTTTTATCTTCAGAAA
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                                                                                                                                                                                                                                                                                                                                              AACAATCGCTGCCCTCTCTGCCAGCAGGACTGGGTGGTCCAAAGAATCGGCAAATGAGAG
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/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_66"
/note="Organ: ovary; Vector: pcMV-SpORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life Technologies. "
126 c 165 g 151 t
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/db_xref="taxon:9606"
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Pred. No. 1.6e-145;
0; Mismatches 6;
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Matches 693
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144 TACGTGCGCCATCTGCAGGGTCCAGGTGATGCCTGTCTTAGATGTCAAGCTGAAAA
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Plate: LLAM10070 row: p column: 21
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 781)
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National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATGTTCTCCCTCAAGAAGTGGAACGCGG-GGCCATGTGGAGCTGGGACGTGGAAGTGCGA
                                                                                                                                                                                                                              CCAAAGAATCGGCAAATGAGAGTGGTTAGAAGGCTTCTTAGCGCAGTTGTTCAGAGCCCCT
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AAATAGGAGCCGATGGATCTGTGGTCCTTTGGGACTCATCAAAGCCTGGGTTTAGCATTT
                             AAATAGGAGCCGATGGATCTGTGGTC--TTTGGACTCAAAGCCTTGGTT--AGCATT
                                                                                                                                                 GGTGGATCTTGTAATCCAGTGCCCTACAAAGGCTAGAACACTACAGGGGATGAATTCTTC
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/clone lib="NNH MGC 86"
/clone lib="NNH MGC 86"
/clone lib="NNH MGC 86"
/note="Organ: bone; Vector: pCMV-SPORT6; Site 1: Not1;
/note="Organ: bone; Vector: pCMV-SPORT6; Site 1: Not1;
Site 2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.533 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH MGC Library."

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tissue_type="osteosarcoma,
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 3.8e-145;
0; Mismatches 23;
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BASE COUNT	FEATURES source	TITLE  JOURNAL  COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 47 AW001261/c LOCUS DEFINITION	04 04 04 04	0
/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMACE:2521212" /tissue_type="colonic mucosa from 3 patients with Crohn's disease" /lab host="DH10B (phage-resistant)" /clone_lib="Soares_Dieckgraefe_colon_NHCD" /note="Organ: colon; Vector: PT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(RI) primer [5' TGTTACCAATCTGAACTGGAACGGCCGCCGTCTTTTTTTT	This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco High quality sequence stop: 456. Location/Qualifiers e 1670			AW(	673 AAGCAGTTTCGAGACTTTTTCGATGCTTATGGTTGATCAGTTAAAAAAGAATGTTACAGT 732	500 TGTCAGTTTTATCTTCAGAAATTCTCTGTGATTAAGAAGA-TAATTTATTAAAGGTGGTC 558
QY  Db  RESULT 48  BG111145  LOCUS  DEFINITION  ACCESSION  VERSION  KEYWORDS  SOURCE  ORGANISM  REFERENCE  AUTHORS  TITLE  JOURNAL  COMMENT	Db Db	Qy Qy	Qy Qy da	оу Оу	Q	Query Match Best Local; Matches 64  Qy 88  Db 670  Qy 148  Db 610
741 AAGTGCAGTTTAAA 754	138 CAAATTGAATCACCTTTATAATTTACCCATTTCTATACAACAGGCAGTGGAAGCAGTTTC 79 683GAGACTTTTCGATGGTTATGGTTGATCAGTTAAAAAAGAATGTTACAGTAACAAATA 740			328 AGAATCGGCAAATGAGAGTGGTTAGAAGGCTTCTTAGCGCAGTTGTTCAGAGCCCTGGTG 387	9 6 5 6	73.4%; Score 553.6; DB 9; Length 670; Similarity 95.0%; Pred. No. 5.3e-145; D; Conservative 0; Mismatches 19; Indels 15; Gaps TTCTCCCTCAAGAAGTGAAACGCGGTGGCCATGTGGAGCTGGAGCTGGAGTGCGATACG

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BASE COUNT
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10024 row: m column: 13
High quality sequence stop: 602.
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                                                                                                                                                                                                                                                     ATCAAAGCCTTGGTT--AGCATTTGTCAGTTTTATCTTCAGAAATTCTCTCTGTGATTAAGA 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATCATTCCTTCCACAACTGCTGCATGTCCCTGTGGGTGAAACAGAACAATCGCTGCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCTCCAAGTCGGGAGGCGACAAGATGTTCTCCCCTCAAGAAGTGGAACGCGGTGGCCATG
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                                                                                                                                                                                                                                                                                                                                                           ATCAAAGCCTTGGTTTAGCATTTTGTCAGTTTTATCTTCAGAAATTCTCTGCGATTAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATCATTCCTTCCACAACTGCTGCATGTCCCTGTGGGTGAAACAGAACAATCGCTGCCCT
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--- CCCATTTCTATACAACAGGCAGTGGAAGCA--GTTTCGAGACTTTTTCGATGCTTAT 702
                                                                   TTAGAAAGTGGCCTTTAAACAACGGAAGAGGCTCCCAATTGCATCACTCGTTTATTAATC
                                                                                                                                       ----AGAAGTGCTATAAAAAAGGAAAGACTCCAAATTGAATCACCTTATAATTTA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACACTACAGGGGATGAATTCTTCAAATAGGAGCCGATGGATCTGTGGTCCTTTGGGACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACACTACAGGGGATGAATTCTTCAAATAGGAGCCGATGGATCTGTGGTC--TTTGGACTC 478
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Location/Qualifiers
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/lab host="DHIOB (phage resistant)"
/clome_lib="NIH MGC_86"
/clome_lib="NIH MGC_86"
/note="Organ: bone; Vector: pCMV-SPORT6; Site 1: NotI;
/note: pCMV-SPORT6; Site 1: NotI;
/note: pCMV-SPORT6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      One="IMAGE: 4369332"
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Pred. No. 6.5e-145;
0; Mismatches 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McCray Lab
University of Iowa
2024 University of Iowa Med Labs,
Tel: 319 356 4866
Fax: 319 356 7171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: M13 FORWARD
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics (www.resgen.com) (www.openbiosystems.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: McCray,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Res. 6 (9),
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Normalization and subtraction: two approaches
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Bonaldo, M.F., Lenno
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                     /clone_lib="UI-CF-DUI"
/clone_Torgan: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: RocR I; Site_2: Not I;
UI-CF-DUI is a normalized cDNA library containing the following tissue(s): Primary Lung Epithelial Cells The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this
                     മ
                                       library is GGCTGTAGGC.
TAG_LIB=UI-CF-DU1
TAG_TISSUB=Lung_Bpithelial Cells
TAG_SEQ=GGCTGTAGGC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="UI-CF-DU1-adr-f-23-0-UI"
/tlssue_type="primary Lung Epithelial Cells"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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mRNA sequence.
BG718227
BG718227.1 GI:139974
EST.
                                                                                                                                                                                                                                                                                                                                      48
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NH
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution informat
                                                                                                                1 (bases 1 to 715)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                   Homo
                                                                                                                                                                                              Homo sapiens (human)
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found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLAM10745 row: 1 column: 23 High quality sequence stop: 714.
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                     ATCAAAGCCTTGGTTTAGCATTTTGTCAGTTTTATCTTCAGAAATTCTCTGCGATTAAGA
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Sequence 7 from Patent WO0175145.
AX282592
Issakani,S.D., Huang,J., Sheung,J. and Pray,T.R. Ubiquitin ligase assay Patent: WO 0175145-A 7 11-OCT-2001;
                                           Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                  Homo sapiens (human)
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AL929565 Mouse DNA
AJ321208 Homo sapi
AC137264 Rattus no
BC0111127 Mus muscu
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                                                                                                                                                                                                                                                                                                     Submitted (10-APR-1999) Lineberger Comprehensive Cancer Center, University of North Carolina at Chapel Hill, Mason Farm Rd. and Manning Dr., Chapel Hill, NC 27599-7295, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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ta,T., Michel,J.J., Schottelius,A.J. and Xiong,Y.

Cl, a homolog of APC11, represents a family of cullin partners th an associated ubiquitin ligase activity

1. Cell 3 (4), 535-541 (1999)
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                                                                                                                                                                                                                                                                                                                                                             Michel, J. and Xiong, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
84 c 108 g 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rmaceuticals, Inc.
Location/Qualifiers
                                                                 QQDWVVQRIGK"
                                                                            /translation="madvedgeetCalashsgssgstsggdkmfslkkmnavammsmd
vecdtcaicrvQvmdaclrcQaenkQedcvvvwgecnhsfhnccmslwvkQnnrcplc
                                                                                                  /codon_start=1
/product="RING finger_protein"
/protein_id="AAD30147.1"
/db_xref="GI:4809218"
                                                                                                                                                                                                                                        ₽.
                                                                                                                                                                                                                                                    organism="Homo sapiens"
mol_type="mRNA"
                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                          note="Cullin partnering igase activity"
                                                                                                                                                                                  gene="ROC2"
                                                                                                                                                                                                            gene="ROC2"
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Pred. No. 6.1e-66;
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124; DB 9;
No. 6.1e-66;
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(ROC2)
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                               Circle, Palo Alto, CA 94303, USA
This CDS clone is a part of a collection of human full length
capturession clones generated by BB Biosciences Clontech and the
Harvard Institute of Proteomics. Each CDS has been cloned in two
forms: with and without stop-codon (to allow fusion with C-terminal
forms: with and without stop-codon (to allow fusion with C-terminal
tag). The CDS has been directionally cloned using BD In-Fusion(TM)
cloning system between the SalI and HindIII sites of the pDNR-DUAL
vector. Additional sequences in the clone: ACC' after SalI site
and before 'ATG' to provide Kozak consensus sequence; 'GG' after
last codon and before HindIII site to maintain reading frame.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 342)
Kalnine, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Koundinya, M., Raphael, J., Moreira, D., Kelley, T., Labrehan, M. and Farmer, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Koundinya, M., Raphael, J., Moreira, D., Phelan, M. and Farmer, A. Cloning of human full-length CDSs in I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BT007348
BT007348.1
                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: http://bioinfo.clontech.com/orfclones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (13-MAY-2003) BD Biosciences Clontech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                                     82
                                                                     QQDWVVQRIGK"
83 c
                                                                                                     /codon_start=1
/product="ring finger protein 7"
/protein_id="AAP36012.1"
/protein_id="AAP36012.1"
/db_xref="G1:30583535"
/translation="MADVEDGEETCALASHSGSSGSKSGGDKMFSLKKWNAVAMWSWD
/translation="MADVEDGEETCALASHSGSSGSKSGGDKMFSLKKWNAVAMWSWD
VECDTCAICRVQVMDACLRCQAENKQEDCVVVWGECNHSFHNCCMSLWVKQNNRCPLC
                                                                                                                                                                                                                                                                       collection"
                                                                                                                                                                                                                               /lab_host="DH5alpha T1 resistant"
/note="Vector: pDNR-Dual"
                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GH00912X1.0"
                                                                                                                                                                                                                                                                                      clone_lib="BD Creator(TM) CDS Library derived from MGC
                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
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100.0%;
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Primates;
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Score 124; DB 9;
Pred. No. 6.1e-66;
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                Length 342;
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PAT 27-AUG-2002

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                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAG:apoptosis sensitivity gratent: JP 2001526063-A 2 11
WARNER LAMBERT CO
OS Unidentified
PN JP 2001526063-A/2
PD 18-DEC-2001
PF 15-DEC-1998 JP 2000525-
PF 19-DEC-1997 US 60/0
YI SUN
PC C11N15/09,A61K31/711,A
PC A61P39/06,
PC A61P39/06,C07K14/47,C0-
PC A61P39/06,C07K14/47,C0-
PC A61P31/00,C07K14/47,C0-
PC G01N33/50,G01N33/68,C1-
Strandedness: Double;
CC Topology: Linear;
CC Topology: Linear;
CC /note = 'Human SAG'
FT CDS
FT CDS
FT CDS
FT Mat Deptide 1.33
FT mat peptide 1.33
FT mat peptide 1.33
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                                                                                                                                    124;
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SAG:apoptosis sensitivity
BD096967
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JP 2001526063-A/2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unidentified
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                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unclassified
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                                                                          CTGC 124
                                                                                                                 CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
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                                                                                                                                                                                                                                                              Conservative
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A61P43/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC
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15-DEC-1998 JP 2000525451
19-DEC-1997 US 60/0681
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                                                                                                                                                                                                                                                                              Score 124; DB 6;
Pred. No. 6.4e-66;
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18-DEC-2001;
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WARNER LAMBERT CO

UNIDEC-2001

PN JP 2001526063-A/24

PD 18-DEC-2001

PF 15-DEC-1998 JP 2000525451

PR 19-DEC-1997 US 60/068179,11-SEP-1998 US 60/099840 PI

YI SUN

PC C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P17/02,A61P35/00,

PC A61P39/06,

PC A61P39/06,

PC A61P43/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC

PC G01N33/50,G01N33/68,C12N15/00,A61K37/02,C12N5/00 CC

Strandedness: Double;

CC Topology: Linear;

CC SAG:apoptosis sensitivity gene

FH Key

Locafic Locafic
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SOURCE
ORGANISM
                                    REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                            DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                          RESULT 6
BD096994
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AUTHORS
TITLE
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ACCESSION
VERSION
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BD096989
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Sun,Y.
SAG:apoptosis sensitivity gene
Patent: JP 2001526063-A 29 18-DEC-2001;
WARNER LAMBERT CO
OS Unidentified
                                                                                                                                unidentified unidentified
                                                                                                                                                                SAG:apoptosis sensitivity gene
BD096994
BD096994.1 GI:22642582
JP 2001526063-A/29.
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                                                                                                               unclassified.
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Similarity 100.0%;
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                                                                                           (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
155 c 201 g 19
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                                                                                           754)
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Pred. No. 6.4e-66;
Nismatches 0;
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<u>.</u>

Gaps

120 260

200 60

PAT 27-AUG-2002

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RESULT 7
BD096995
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KEYWORDS
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ACCESSION
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Best Local S
Matches 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
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WARKIER LAWRES LAWRES CO.

OS Unidentified

PN JP 2001536063-A/30

PD 18-DEC-2001

PF 15-DEC-1998 JP 2000525451

PF 19-DEC-1997 US 60/068179,11-SEP-1998 US 60/099840 PI

YI SUN

PC C12015/09,A61K31/711,A61K38/00,A61K48/00,A61P17/02,A61P35/00,

PC A61P39/06,

PC A61P3/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC

PC G01N33/50,G01N33/68,C12N15/00,A61K37/02,C12N5/00 CC

Strandedness: Double;

CC T0p0109y: Linear;

CC SAG:apoptosis sensitivity gene

FT CDS

1. 339

FT CDS

1. 339.
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SAG:apoptosis sensitivity 9
BD096995.1 GI:22642583
JP 2001526063-A/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207
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A61P43/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21
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1, .754
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Pred. No. 6.4e-66;
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Duan,H., Tsvetkov,L.M., Liu,Y., Song,Y., Swaroop,M., Wen,R., Kung,H.F., Zhang,H. and Sun,Y.

Promotion of S-phase entry and cell growth under serum starvation by SAG/ROC2/Rbx2/Hrt2, an E3 ubiquitin ligase component: association with inhibition of p27 accumulation

Mol. Carcinog. 30 (1), 37-46 (2001)
                                                                                                                                           growth, but not for germination: chip profiling implicates in cell cycle regulation Oncogene 19 (24), 2855-2866 (2000)
                                                                                                                                                                                                                                      Expression, purification, and biochemical characterization a RING finger redox-sensitive protein Free Radical Biol. Med. 27, 193-202 (1999)
4 (bases 1 to 754)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Duan, H., Wang, Y., Aviram, M., Swaroop, M., Loo,
Tian, Y., Mueller, T., Bisgaier, C.L. and Sun, Y.
SAG, a novel zinc RING finger protein that pr
apoptosis induced by redox agents
Mol. Cell. Biol. 19 (4), 3145-3155 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eucheria; Primates;
1 (bases 1 to 754)
Duan, H., Warr "
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the RING finger domain for apoptosis protection
Carcinogenesis 20 (10), 1899-1903 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sun,
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                                                                                                                                                                                             Yeast homolog of human SAG/ROC2/Rbx2/Hrt2 is essential for
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                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                                                                                          Direct Submission
Submitted (25-MAY-2001) National Institutes of Gene Collection (MGC), Cancer Genomics Office, Gene Collection (MGC), Cancer January (MGC), Bethescinstitute, 31 Center Drive, Room 11A03, Bethescinstitute, 31 Center Drive, 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens, ring finger protein 7, mRNA, complete cds.
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Submitted (16-SEP-1998) Department of Molecular Biology,
Parke-Davis, 2800 Plymouth Rd, Ann Arbor, MI 48105, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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Mammalia; Eutheria;
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Sequencing Center
                                                                                                                                                                        Contact: MGC help desk
                                                                                                                                                                                                   NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                               Strausberg, R
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/note="redox sensitive, metal binding;
cells from apoptosis induced by redox c
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/protein id="AAD25962.1"
/db_xref="G1:4588034"
/tzanslation="MADVEDGEETCALASHSGSSGSKSGGDKWFSLKKWNAVAWWSWD
VECDTCAICRVQVMDACLRCQAENKQEDCVVVWGECNHSFHNCCMSLWVKQNNRCPLC
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Pred. No. 6.4e-66;
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SOURCE
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BC005966
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                                                                AUTHORS
TITLE
JOURNAL
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Best Local Similarity
    REMARK
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BC005966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk,
A.M., Holloway, M., Telford, B, Hodgson, A., B
Muzny,D.M., Gibbs,R.A.
USA NIH-MGC Project URL: http://mgc.nci.nih.
                                                           Direct Submission
Submitted (02-APR-2001) National Institutes
                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 822)
                                                                                                                                                       Homo sapiens (human)
                                                                                                                                                                                          MGC
                                                                                                                                                                                                                                     mRNA, complete cds.
                                                                                              Strausberg, R.
                                                Gene Collection (MGC),
                                                                                                                                                                                                     BC005966.1 GI:13543635
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                                 Institute,
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178 c
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1p/19q loss"
/clone_lib="NOI_CGAP_Brn67"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="Vector: pCMV-SPORT6"
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                                 31 Center Drive,
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                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 6.5e-66;
                                                 Cancer
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                      Genomics Office, National
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, A., Bouck,
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                                                                                                                                                                                                                                                  IMAGE: 4069078,
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                                                                Mammalian
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SOURCE
ORGANISM
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AF164679
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                       TITLE
                                                 AUTHORS
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Best Local
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                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 836)
Son,M.Y., Park,J.W., Kim,Y.S., Kang,S.W., Marshak,D.R., Park,W. ar
                                                                                                                                                                                                                                                                                                                                                                                                                  Ц
Protein kinase CKII interacts with and phosphorylates protein containing ring-H2 finger motif
                                   Bae,Y.S.
                                                                                                        Homo sapiens
                                                                                                                       Homo sapiens (human)
                                                                                                                                                  AF164679.1 GI:5917673
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AF164679
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http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be for through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 21 Row: o Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                        CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue_type="Kidney, hypernephroma"
/clone_lib="NIH_MGC_58"
/lab_host="DH10B"
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|mol_type="mRNA"
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Pred. No. 6.5e-66;
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10512750
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AL Patent: JP 2001526063-A 23 18-DBC-2001;

WARNER LAMBERT CO
OS Unidentified
PN JP 2001526063-A/23
PD 18-DBC-2001
PF 15-DBC-1998 UP 2000525451
PF 19-DBC-1997 US 60/068179,11-SEP-1998 US 60/099840 PI
YI SUN
PC C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P17/02,A61P35/00,
PC A61P39/06,
PC A61P39/06,
PC A61P39/06,GO1N33/68,C12N15/00,A61K37/02,C12N1/19,C12N1/21 PC
Strandedness: Double;
SC TSC-1707, Linear.
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                                                                                                                                                                                                                                                                                                                                                                  unidentified
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JP 2001526063-A/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 836)
Son, M.-Y., Park, J.-W.,
and Bae, Y.-S.
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                                                                                                                                                                                                                                                                                                                              (bases 1 to 754)
                  Topology: Linear;
SAG:apoptosis sensitivity
                                                                                                                                 C12N15/09, A61K31/711, A61K38/00, A61K48/00, A61P17/02, A61P35/00
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Location/Qualifiers
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185 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biophys. Res.
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product="ring finger protein CKBBP1"
protein id="AAD55984.1"
db_xref="G1:5917674"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 6.5e-66;
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REFERENCE
AUTHORS
TITLE
JOURNAL
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SOURCE
ORGANISM
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ACCESSION
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BD096981
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ORIGIN
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ORIGIN
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Best Local
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                                        Matches 116;
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                                                                                                                                                                    SAC:apoptosis sensitivity gene
SAC:apoptosis sensitivity gene
AL Patent: JP 2001526063-A 16 18-DEC-2001;

PARNER LAMBERT CO
OS Unidentified
PD 19-2001526063-A/16
PD 18-DEC-2001
PF 15-DEC-1998 JP 2000525451
PF 15-DEC-1997 US 60/068179,11-SEP-1998 US 60/099840 PI
YI SUN
PC C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P17/02,A61P35/00,
PC A61P39/06,
PC A61P39/06,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC
PC G01N33/50,G01N33/68,C12N15/00,A61K37/02,C12N5/00 CC
Strandedness: Double;
CC Topology: Linear;
CC Topology: Linear;
CC SAG:apoptosis sensitivity gene
FH Key
CDS 1. 339
FT CDS
PT CDS
PT CDS
PT mat peptide 1. 339.
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BD096981
SAG:apoptosis sensitivity gene
BD096981
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JP 2001526063-A/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                            unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        unidentified
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                                     93.5%; Sc
llarity 100.0%; F
Conservative 0;
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A61P39/06,
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100.0%; Pr/
0;
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ide 1. .339.
tion/Qualifiers
                                    Score 116; DB 6; 1
Pred. No. 6.6e-61;
0; Mismatches 0;
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Pred. No.
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                                                            Length 754;
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                                     Indels
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Patent: JP 2001526063-A 22 18-DEC-2001;

WARNER LAMBERT CO

UNIDECTOR

PR 19-DEC-1998 JP 2000525451

PR 19-DEC-1997 US 60/068179,11-SEP-1998 US 60/099840 PI

PC C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P17/02,A61P35/00,

PC A61P39/06,

PC A61P39/06, CO7K14/47,CO7K16/18,C12N1/15,C12N1/19,C12N1/21 PC

PC C011N3/50,C01N3/68,C12N15/00,A61K37/02,C12N1/21 PC

Strandedness: Double;

CC SAG:apoptosis sensitivity gene

FH Key

FT CDS

FT mar -
                   REFERENCE
AUTHORS
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SOURCE
ORGANISM
                                                        SOURCE
ORGANISM
                                                                              DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                 RESULT 15
BD096982
LOCUS
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AUTHORS
TITLE
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ACCESSION
VERSION
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BD096987
LOCUS
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ORIGIN
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       TITLE
                                                                                                                                                                                                                                                                                                Matches 112;
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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Sun, Y.
SAG: apoptosis sensitivity gene
                                                                               BD096982
BD096982.1 GI:22642570
JP 2001526063-A/17.
                                                        unidentified unidentified
                                                                                                                  BD096982
SAG:apoptosis sensitivity
                                           unclassified
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ilarity 100.0%;
Conservative (
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peptide 1. .339.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                            /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
153 c 202 g 19
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                                754)
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Pred. No. 2.1e-58;
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BASE COUNT
ORIGIN
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BD096983
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TITLE
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WARNER LAMBERT CO
OS Unidentified
PN JP 2001526663-A/17
PD 18-DEC-2001
PF 15-DEC-1998 JP 200525451
PF 19-DEC-1997 US 60/068179,11-SEP-1998 US 60/099840 PI
YI SUN
PC C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P17/02,A61P35/00,
PC A61P39/06,
PC A61P39/06,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC
C12N5/10,C12Q1/68,
PC A61P43/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC
C12N5/10,C12Q1/68,
PC G01N33/50,G01N33/68,C12N15/00,A61K37/02,C12N5/00 CC
Strandedness Double;
CC Topology: Linear;
CC Topology: Linear;
CC SAG:apoptosis sensitivity gene
FH Key
FT CDS
PT Mat_Deptide 1.339.
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           Sun,Y.

SAG:apoptosis sensitivity gene
SAG:apoptosis sensitivity gene
Patent: JP 2001526063-A 18 18-DEC-2001;

WARNER LAMBERT CO
OS Unidentified
PN JP 2001526063-A/18
PD 18-DEC-2001
PF 15-DEC-1998 JP 2000525451
PF 15-DEC-1997 US 60/068179,11-SEP-1998 US 60/099840
PR 19-DEC-1997 US 60/068179,11-SEP-1998 US 60/099840
PC C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P17/02,A61P
PC A61P39/06,
PC A61P39/06,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/2
PC A61P43/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/2
PC G01N3)50,G01N33/68,C12N15/00,A61K37/02,C12N5/00 CC
Strandedness: Double;
CC Topology: Linear;
CC SAG:apoptosis sensitivity gene
FH Key
FT CDS
PT CDS
PT mat_Deptide
1. 339
PT mat_Deptide
1. 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                             unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unidentified
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JP 2001526063-A/18.
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SAG:apoptosis sensitivity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGTTGTGGTCTGGGGAGAATGTAATCATTCCTTCCACAACTGCTGC 124
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A61P43/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC
                                                                                                                                                                                                     C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P17/02,A61P35/00
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 peptide 1. .339
Location/Qualifiers
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/mol_type="genomic_DNA"
/db_xref="taxon:32644"
_155 c 201 g 19
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/ gene.
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BD096986
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ACCESSION
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Best Local Similarity
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Best Local Similarity
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AL Patent: JP 2001526063-A 21 18-DEC-2001;
WARNER LAMBERT CO
OS Unidentified
PN JP 2001526063-A/21
PP 18-DEC-1998 JP 2000525451
PF 15-DEC-1998 US 60/068179,11-SEP-1998 US 60/099840
PR 19-DEC-1997 US 60/068179,11-S
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JP 2001526063-A/21.
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SAG:apoptosis sensitivity
BD096986
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                                                                                                                                   CGATAČGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
                            AAACAAACAAGAGGACTGTGTGTGTGGGTCTGGGGAGAATGTAAT 103
                                                                                               CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAGATGTCAAGCTGA
AAACAAACAAGAGGACTGTGTTGTGGTCTGGGGAGAATGTAAT
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Conservative (
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
155 c 201 g 19
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                                                                                                                                                                                                                     Score 103; DB 6; 
; Pred. No. 9e-53;
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Pred. No. 2.8e-55;
0; Mismatches 0;
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gene.
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BD096985
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ACCESSION
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BD096990
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ORGANISM
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KEYWORDS
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Best Local Similarity
                                                                                              JOURNAL
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 SAG: apoptosis sensitivity gene
Patent: JP 2001526063-A 20 18-DEC-2001;
WARNER LAMBERT CO
OS Unidentified
PN JP 2001526663-A/20
PD 18-DEC-2001
PF 15-DEC-1998 JP 2000525451
PR 19-DEC-1997 US 60/068179,11-SEP-1
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PN JP 2001525063-A/2:
PD 18-DEC-2001
PF 15-DEC-1998 JP 20:
PR 19-DEC-1997 US
YI SUN
PC C12N15/09,A61K31/-
PC A61P3/00,C07K14/-
,C12N5/10,C1201/68,
PC G01N33/50,G01N33/-
Strandedness: Double;
CC Topology: Linear;
CC SAG:apoptosis sen:
FH Key
FT CDS
FT CBS
FT mat_peptide 1
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BD096985.1 GI:22642573
JP 2001526063-A/20.
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BD096990
BD0969901 GI:22642578
JP 2001526063-A/25.
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SAG:apoptosis sensitivity gene
                                                                                                                                                        unclassified
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JP 2001526063-A/20 .
18-DEC-2001
15-DEC-1998 JP 2000525451
19-DEC-1997 US 60/068179,11-SEP-1998 US
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Key Location/Qualifiers
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A61P39/06,
A61P43/00, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21 PC
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19-DEC-1997 US 60/068179,11-SEP-1998 US
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/mol_type="genomic_DNA"
/db_xref="taxon:32644"
152 c 202 g 19
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Location/Qualifiers
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Pred. No. 9e-53;
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BD096973
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Best Local S
Matches 97
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PD 18-DEC-2001
PP 15-DEC-1998 JP 2000525451
PP 15-DEC-1998 US 60/068179,11-SEP-1998 US 60/09984(
PR 19-DEC-1997 US 60/068179,11-SEP-1998 US 60/09984(
PR 19-DEC-1997 US 60/068179,11-SEP-1998 US 60/09984(
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PC A61P39/06,
PC A61P39/06,
PC A61P43/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/19,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12N5/10,C12
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PC A61P3/50, G01N3/68,
PC G01N3/50, G01N3/68, C12N15/00, A61K37/02, C12N5/00 CC
Strandedness: Double,
CC Topology: Linear;
CC Topology: Linear;
CC SAG: apoptosis sensitivity gene
FH Key
FT CDS
FT CDS
1. 339
FT mat_peptide 1. 339.
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                                                                                          /organism="unidentified"
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                            /db_xref="taxon:32644"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (09-OCT-2000) Molecular Biology, Pfizer Global Research and Development, 2800 Plymouth Road, Ann Arbor, MI 48105, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Swaroop,M., Gosink,M. and Sun,Y.
SAG/RCC2/Rbx2/Hrt2, a component of SCF E3 ubiquitin ligase: genomic structure, a splicing variant, and two family pseudogenes DNA Cell Biol. 20 (7), 425-434 (2001)
21398045
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Tian, Y., Mueller, T., Bisgaier, C.L. and Sun,
SAG, a novel zinc RING finger protein that
apoptosis induced by redox agents
Mol. Cell. Biol. 19 (4), 3145-3155 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sun, Y.
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AF312226
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    AATGTAATCATTCCTTCCACAACTGCTGC 124
                                          ATGCCTGTCTTAGATGTCAAGCTGAAAACAAACAAGAGGACTGTGTTGTGGTCTGGGGGAG
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                                                                                                                                                                                                                                                                                                                                                                                             activity as a component
                                                                                                                                                                                                                                                                                                            /protein_id="AAK37450.1"
/db_xref="GI:13649606"
                                                                                                                                                                                                                                                                                                                                                    product="SAG splice variant"
                                                                                                                                                                                                                                                                                                                                                                                                                note="SAG-v; lacks zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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/db_xref="taxon:9606"
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                                                                                                                                                               Length 674;
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un.Y.
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; Homo.
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                                                           REFERENCE
AUTHORS
TITLE
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ACCESSION
VERSION
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BD096992
LOCUS
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ORGANISM
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BD096984
LOCUS
DEFINITION
ACCESSION
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KEYWORDS
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ORGANISM
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TITLE
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PN JP 200152663-A/19
PD 18-DEC-2001
PP 15-DEC-1998 JP 2000525451
PF 15-DEC-1998 US 60/068179,11-SEP-1998 US 60/099840
YI SUN
PC C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P17/02,A61F
PC A61P39/06,
PC A61P39/06,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/2
PC A61P39/06,C07K14/47,C07K16/18,C12N1/15,C12N1/29,C12N1/2
PC A61P39/06,C07K14/47,C07K16/18,C12N1/15,C12N1/29,C12N1/2
PC A61P39/06,C07K14/47,C07K16/18,C12N1/15,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12N1/29,C12
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                                                                                                                                                                                                                                                                                                                                                                                                                102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 GTCTTAGATGTCAAGCTGAAAAAAAAAAAGAGGACTGTGTTTGTGGTCTGGGGAGAATGTA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83;
SAG:apoptosis sensitivity gene
Patent: JP 2001526063-A 27 18-
WARNER LAMBERT CO
OS Unidentified
                                                                                                                                              unidentified
unidentified
                                                                                                                                                                                   BD096992.1 GI:22642580 JP 2001526063-A/27.
                                                                                                                                                                                                                           SAG:apoptosis sensitivity gene. BD096992
                                                                                Sun,Y.
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                                                                                                                           unclassified.
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WARNER LAMBERT CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                        ATCATTCCTTCCACAACTGCTGC 264
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A61P43/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21
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                                                                                                    754)
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Pred. No.
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                                        18-DEC-2001;
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PAT 27-AUG-2002

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60/099840 PI

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ACCESSION
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BD096991
LOCUS
                                                                                                  FEATURES
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ORIGIN
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PD 18-DEC-1998 JP 2000525451

PF 19-DEC-1998 JP 2000525451

PR 19-DEC-1998 US 60/068179,11-SEP-1998 US 60/099840 PI

YI SUN

PC C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P17/02,A61P35/00,

PC A61P39/06,

PC A61P43/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC

PC A61P43/00,G01N33/68,C12N15/00,A61K37/02,C12N5/10,C12Q1/68,

PC G01N33/50,G01N33/68,C12N15/00,A61K37/02,C12N5/00 CC

Strandedness: Double;

CC Topology: Linear;

CC SAG:apoptosis sensitivity gene

FH Key

Tous

Transition/Qualifiers

FT CDS

Transition/Cualifiers

FT CDS

Transition/Cualifiers

Transition/Cualifiers
                                                                                                                             OS Unidentified
PN JP 2001526063-A/26
PD 18-DEC-2001
PF 15-DEC-1998 JP 2000
PF 15-DEC-1997 US
YI SUN
PC C12N15/09, A61K31/71
PC A61P39/06,
PC A61P39/06,
PC G01N33/50,G01N33/68,
PC G01N33/68,
PC G01N33/50,G01N33/68,
PC G01N33/68,
PC G01N33/68,
PC G01N33/68,
PC G01N33/68,
PC G01N33/68,
PC G01N3/
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SAG:apoptosis sensitivity gene
Patent: JP 2001526063-A 26 18-DEC-2001;
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SAG:apoptosis sensitivity gene.
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A61P43/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                               SAG:apoptosis sensitivity gene
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L9-DEC-1997 US 60/068179,11-SEP-1998 US
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organism="unidentified"
/mol_type="genomic DNA"
                                                                                           ocation/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
155 c 201 g 19
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1. .339.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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RESULT 26
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ACCESSION
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                                                                                                                                                                                                                                                                                                                                      OS Unidentified
PN JP 2001526063-A/28
PD 18-DEC-2001
PF 15-DEC-1998 JP 2000525451
PF 15-DEC-1998 US 60/068179,11-SEP-1998 US 60/099
YI SUN
PC C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61D17/02,A
PC A61P39/06,
PC A61P43/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N
,C12N5/10,C12Q1/68,
PC G01N33/50,G01N33/68,C12N15/00,A61K37/02,C12N5/00 CC
Strandedness: Double;
CC Topology: Linear;
CC SAG:apoptosis sensitivity gene
FM Key
FT CDS
1.339
FT mat_peptide / 1.339
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SAG:apoptosis sensitivity
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A61P43/00, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21
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155 c 201 g
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                       Bayl
                                                                                                                                                                                       Submitted (25 MAY-2002) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                      Baylor Plaza, Houston, 3 (bases 1 to 35638) Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                     Submitted (24-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                 Submitted (30-JUL-2002)
                                                                                                                                                                Baylor Plaza, Houston, 4 (bases 1 to 35638)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wu, Y.F., Zhou, J., Gibbs, R.
                                                                                                              Direct Submission
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AC112771.6 GI:22003982
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 35638)
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                       Human Genome Sequencing
Genetics, Baylor College
TX 77030, USA
                                                 Center, Department of Medicine, One
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Direct Submission
Submitted (28-SEP-2002) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
On Jul 30, 2002 this sequence version replaced gi:20976460.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
gc-help@bcm.tmc.edu
                                                                                                                                                                                    Department
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sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing. CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only

STSs are identified using ePCR (Genome Res. of a local database that includes entries from local mapping efforts. dbsTs, 7:541-550) searches

Repeats are identified using RepeatMasker (A. Smit and P. Green

unpublished.) for Human and Mouse Bequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht

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   /rpt_family="AluSg/x"
3643. .3758
                                complement (3541.
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                 standard_name="SHGC-105132"
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chromosome="3"
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                                                                                                                                                                                                                                                                                                                               function="clone overlap"
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RESULT 27
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AC068693.2 GI:8139716
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
Homo sapiens
                                                          Homo sapiens
SEQUENCE, 25
                                                                                 AC068693
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RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Raderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Burkett, G., Sanderson, S., Baldwin, J., Barna, N., Burkett, G., Collins, S., Coungeplarok, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Galagan, J., Gardyna, S., Ginde, S., Heaford, A., Horton, L., Graham, J., Lancore, N., Johnson, R., Jones, G., Kann, L., Karatas, A., Klein, J., Lancore, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Comnor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vonnis, C., Minselon, J., Zimmer, A., and Zody, M., Myman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A., and Zody, M.
                                                                                                                                                Submitted (06-MAY 2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 1, 2000 this sequence version replaced gi:7712215.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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Sequencing vector: M13; M79815; 100% of reads Sequencing vector: M13; M79815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 112098 bases at least Q40 Consensus quality: 112098 bases at least Q30 Consensus quality: 121119 bases at least Q20 Insert size: 158000; agarose-fp Insert size: 122641; sum-of-contigs Quality coverage: 3.8 in Q20 bases; agarose-fp Quality coverage: 4.9 in Q20 bases; sum-of-contigs consists of 25 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence NOTE: This is a 'working draft' sequence. It current. as soon as it be preserved. it is available and the accession number will 1119: 3013: 3113: 5008: 5108: 1019: contig gap of contig gap of contig gap of contig contig of 1019 gap of 100 bp of 100 bp g of 1894 bp in length of 100 bp g of 1895 bp in length of 100 bp g of 2046 bp in length 100 bp of 3151 100 bp ďq đđ in length in length sum-of-contigs It currently

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30218: contig of 4330 bp in length
30318: gap of 100 bp
33343: contig of 3025 bp in length
33443: gap of 100 bp
36428: contig of 2985 bp in length
36528: gap of 100 bp
40028: contig of 3500 bp in length
41028: gap of 100 bp
40128: gap of 100 bp
52470: gap of 100 bp
5252: contig of 6727 bp in length
6252: contig of 4399 bp in length
6252: contig of 5483 bp in length
6252: gap of 100 bp
70768: contig of 5483 bp in length
70868: gap of 100 bp
707768: contig of 5216 bp in length
70868: gap of 100 bp
914528: gap of 100 bp
94628: contig of 8216 bp in length
95200: gap of 100 bp
94628: contig of 8353 bp in length
95500: gap of 100 bp
94628: contig of 10672 bp in length
95500: gap of 100 bp
94628: contig of 10672 bp in length
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
Rattus norvegicus
Rattus norvegicus
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238330 bp DNA linear HTG 13-MAY.
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30319. .33343
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33444. .36428
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Pred. No. 8.1e-19;
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Hermander R., Hinges S., Hladen, S.L., Hödgson, A., Houses M.,
Holling B., Hewells S., Haldyn, S., Lhme, J., dickind, D., Jakton, A.,
Jakton, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Lawis, L., Li, Z., Liu, J., Liu
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JOURNAL REFERENCE

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Best Local
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RS Muzny, D. Marie. Mctker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Bardakin, D., Bardaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Balair, J., Blankenburg, K., Blyth, P., Brown, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Biswalo, K., Barnstead, M., Benahmed, F., Bryant, N., Barnstead, M., Barnstead, M., Carder, M., Carter, K., Cavazos, I., Ceassar, H., Center, A., Chen, G., Chen, G., Chen, R., Chen, F., Canderon, E., Chen, G., Chen, G., Chen, R., Canderon, C., Coyle, M., Cree, A., D'Souza, L., Chen, J., Chen, G., Chen, R., Chen, Z., Chu, J., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, R., Chen, Z., Coyle, M., Cree, A., D'Souza, L., Dedardo, O., Derson, S., Daramco, C., Ding, Y., Dinh, H., Divya, K., Detyon, A., Bayes, K., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C., A., Falts, T., Fan, G., Franser, C., M., Eugene, C., Evans, C., A., Foster, M., Garza, M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Guevara, W., Gunaratne, P., Haaland, W., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Haves, A., Henderson, N., Hernandez, J., Jackson, A., Hernandez, J., Jackson, L., Johnson, R., Johnson, C., Liu, J., Karpathy, S., Kally, S., Khan, Z., King, L., Liu, J., Levan, J., Levan, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 GATGCCTGTCTTAGATGTCAAGCTGAAAACAAACAAGAGGACTGTGTTG
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Rattus norvegicus clone
unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.)
NOTE: This is a 'working draft' sequence. It currently
consists of 3 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64585 a
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236157
237214
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53668 c 53820 g
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/db_xref="taxon:10116"
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Pred. No.
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1e CH230-23C21,
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WORKING DRAFT SEQUENCE, 4
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Mangum B., Magua, P., Martin, K., Martin, R., Martinez, E.,
Mangum B., Magua, P., Martin, K., Martinez, R.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Milosavljevic, A., Miner, G., Minja, E., Mortemayor, J., Moore, S.,
Milosavljevic, A., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
Morgan, M., Morris, R., Morris, S., Murphy, M., Nair, L.,
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Mankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
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Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C.,
Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L.,
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Plopper, F., Paul, H., Perez, A., Perez, L., Fanikoch, C.,
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Plopper, F., Paul, H., Perez, A., Perez, L., Primus, E., Paul, J., Shethy, J., Sarethy, R., Sosa, J.,
Shetty, J., Sharatsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,
Shetty, J., Sharatsbeyn, A., Sisson, I., Satter, C.D., Smajs, D.,
Shety, J., Sharatsbeyn, A., Sharatsbeyn, J., Walter, B., Wang, J.,
Walliams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K.,
Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K.,
Walliams, G., Willson, R., Walley, B., Weinston, S., Yen, J., Yoon, L., Yoon, V.,
Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhoo, S., Dunn, D., Yoon, V.,
Weinston, G., Sharatsbeyn, S., Smith, D.R., Holt, R.A., Smith, H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Maylor Plaza, Houston, TX 77030, USA On May 10, 2003 this sequence version replaced gi:24819573. On May 10, 2003 this sequence version replaced gi:24819573. On May 10, 2003 this sequence version replaced gi:24819573. On May 10, 2003 this sequence version replaced gi:24819573. On May 10, 2003 this sequence version replaced gi:24819573. On May 10, 2003 this sequence reads assembled using Atlas and whole genome shotgun sequence ontigy seaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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J., Lu, X., Ma. J., Maheshwari, M., Mahindartue, M., Mahmoud, M., Malloy, K., Manmangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
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Rat Genome Sequencing Consortium.
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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* Consists of 4 contigs. The true order of the pieces
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Center clone name: CH230-23C21
Center clone close clone clon
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Center code: BCM
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A.,
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KEYWORDS
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Charna, N., Camarata, J., Campopiano, A., Chang, J., Boukhgalter, B., Brown, A., Colangelo, M., Collins, S., Collymore, A., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cook, A., Cooke, P., Pitzhugh, W., Gage, D., Galagan, J., Gardyna, Gande, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
                                                                                                                                                                                                                                                                Mammalia; Eutheria; Rodentia; Sciurognathi; Mu
1 (bases 1 to 187353)
Birren, B., Linton,L., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-200C17
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Mus musculus clone RP23-200C17,
                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
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                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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69231. .103385
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5617. .6729
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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5616: gap of unknown length
242823: contig of 237207 bp in length
242923: gap of unknown length
243958: contig of 1035 bp in length
243968: gap of unknown length
244968: gap of unknown length
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Pred. No. 8.5e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: L19568
Center clone name: 200 C 17
Center clone name: 200 C 17
Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 184259 bases at least Q40
Consensus quality: 185710 bases at least Q30
Consensus quality: 186169 bases at least Q20
Insert size: 194000; aggrose-fp
Insert size: 194000; aggrose-fp
Insert size: 186433; sum-of-contigs
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the accession number will be preserved.
1 629: contig of 629 bp in length
630 729: gap of 100 bp
730 750: contig of 21 bp in length
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                                    /mol_type="genomic DNA
/db_xref="taxon:10090"
/clone="RP23-200C17"
                                                                                                                                     organism="Mus musculus"
                                                                                                                                                                                                              ocation,
                                                                                                                                                                                                                         6908: Sorting of 3566 bp in length
7008: gap of 100 bp
14434: conting of 7426 bp in length
14534: gap of 100 bp
32181: conting of 17647.bp in length
32281: gap of 100 bp
51167: conting of 18866 bp in length
51267: gap of 100 bp
72870: conting of 21603 bp in length
72970: gap of 100 bp
149992: conting of 77022 bp in length
150092: gap of 100 bp
187353: conting of 37261 bp in length
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_lib="RPCI-23 Female Mouse BAC"
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REFERENCE
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VERSION
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BD077705
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5'EST of secreted protein expressed
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Edwards, J.B.D.M., Duclert, A. and Lacroix, B.
5'EST of secreted protein expressed in muscles
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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01-AUG-1997 US 08/9051
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JP 2001512016-A/291
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1 (bases 1 to 59155)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 18, clone RP11-352C3
                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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RESULT 32 AC104983

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Matches

BASE COUNT ORIGIN

FEATURES

REFERENCE AUTHORS TITLE

SOURCE

ORGANISM

KEYWORDS VERSION ACCESSION DEFINITION **FOCUS** 

REFERENCE

JOURNAL

AUTHORS

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Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
Submitted (22-DEC-2001) Whitehead Institute/MIT Center for Genome Research, 30 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                be preserved
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Center clone name: 352_C_3
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Schupback, R.,
Stojanovic, N.,
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22873: gap of 100 bp
23723: contig of 766 b)
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24489: contig of 765 b)
24599: gap of 100 bp
25554: contig of 7720 b)
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27043: contig of 757 b)
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27097: contig of 719 b)
28753: gap of 100 bp
28752: contig of 747 b)
30519: gap of 100 bp
305274: contig of 727 b
33736: contig of 729 b
3883: gap of 100 bp
37711: gap of 100 bp
37721: gap of 100 bp
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Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 162304 bases at least Q40
                                                                                                                                                                                                                      Direct Submission
Submitted (24-JAN-2002) Genome Sequencing Center, Washington
Submitted (24-JAN-2002) Genome Sequencing Center, Washington
Oriversity School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                   43;
                                                                                                                                                     Center: Washington University Genome Center code: WUGSC
                                                                                                                                                                                                   University School of Medicine, 4444 Forest Park Parkway, St
MO 63108, USA
On Jan 30, 2002 this sequence version replaced gi:18308830
                                                                                                                                                                                                                                                                       2 (bases 1 to 163521) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 163521)

Waterston,R.H.
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Homo sapiens chromosome 4 clone
SEQUENCE, 4 unordered pieces.
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HTG; HTGS_PHASE1; HTGS_1
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Kaul, R.K., Olson, M.V., Raymond, C., Haugen, E.D.
                                                                                                                                                                                                                                                                          Homo sapiens chromosome 3 clone RP11-229A12, complete sequence AC092418 AC016923 AC092418.3 GI:27228861
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Insert size: 161221; sum-of-contigs
Quality coverage: 8.88 in Q20 bases; agarose-fp
Quality coverage: 8.85 in Q20 bases; sum-of-contigs
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                                                         Unpublished
                                                                                                                1 (bases 1 to 164500)
Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A.,
Saenphimmachak,C., Buckley,D., Kibukawa,M.,
                                                                                                                                                                            Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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112803. 163521
/note="assembly_name:Contig27"
, 32426 c 33346 g 46399 t
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89085._.112702
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/mol type="genomic DNA"
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/chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_name:Contig28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="assembly_name:Contig25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'clone="RP11-210010"
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1664: gap of unknown length
88984: contig of 87320 bp in length
899084: gap of unknown length
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Pred. No. 4.7e-15;
                                                                                                                                                                                                                                                                                                                                        164500 bp
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                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                  Clendenning, J., Ivey, R.G.
                                                                                                                                                                                                                                                                                                                                            DNA
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (18-DEC-2002) Genome Center, University of Washington, Box 352145, Seattle, M 98195, USA On Dec 18, 2002 this sequence version replaced gi:21166206.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Box 352145, Seattle, WA 98195, U 4 (bases 1 to 164500) Kaul, R.K., Olson, M.V., Zhou, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Box 352145, Seattle, WA 98195, USA 3 (Chases 1 to 164500) Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Saenphimmachak,C., Phelps,K.A., Buckley,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Saenphimmachak, C., Buckley, D., Kibukawa, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (24-MAY-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (04-JUL-2001) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Sequencing vector: unknown; 49% of reads
Sequencing vector: plasmid; 51% of reads
Chemistry: Dye-terminator ET; 48% of reads
Chemistry: Unknown; 0% of reads
Chemistry: Dye-terminator Big Dye; 51% of reads
Chemistry: Dye-terminator Big Dye; 51% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 164200 bases at least Q40
Consensus quality: 164447 bases at least Q30
Consensus quality: 164498 bases at least Q20
Insert size: 164500; sum-of-contigs
Quality coverage: 7.7x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haugen, E.D.
                                                                                                                                                                                                                                                                                                                                                   Center project name: chr-3
Center clone name: RP11-229A12 (bc0315)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.genome.washington.edu
Contact: uwgchtgs@u.washington.edu
Drafting Center: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: University of Washington Genome Center Center Code: UWGC
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                                                                                                                                                                                                                                                                                                                        -- Summary Statistics
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Raymond, C.
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Overlapping Sequences: 5': RP11-120C2 (U

ω .. RP11-120C2 (UWGC:bc0239) AC121250, RP11-755B10 (UWGC:bc0671) AC114480 4576-bp overlap

Sequence Quality Assessment:
This entry has been annotated with sequence quality
This estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible GenBank flat file format but are available as part of this entry's ASN.1 file. from zero

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all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phr quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest This sequence was finished as follows unless otherwise noted: restriction digest Phred

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint ance do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

15160     14802     1701     1643     761       2025     1971     390     <800     441       1905     1898     1946     1902     5627       1412     1386     101     <800     7715       3186     3147     637     <800     11604       6226     6297     312     <800     2582       4066     4085     2950     2966     3227       1785     1764     1884     1902     4021       133     <800     4779     4731     2721       5971     5982     5304     5321     6232       3070     3147     12363     12136     4125	118 <800	15 <800 301 <800 6455 6537	3147 1111 2451		3372 3414 2956 2966	19446 19781 11580 11448 2689 	4994 1929 1902	4056 4085 512 <800 7354	6 <800 65382 6597 2067	8696 8826 826 813 4194	EcoRI HindIII Bg
<800 <800 5729 7683 111214 2697 3413 4204 2866 6239	1122 4633 <800 <800	<800 3413 8082	<800 4633 4800	3564	5729	2866 3735	1424	7474 13505	2161	4490	BglII lap FngrPrnt
Version    D0959/4.1	Oy 47 AGATGTCAAGCTGAAAACAAAACAAGAGGACTGTGTTGTGGTCT 89	Query Match Best Local Similari Matches 43; Cons	/CICOMOSOME="3" /CIONE="RP11-229A12" /CIONE= Iib="RPCI human BAC library 11" /clone lib="RPCI human BAC library 11" /note="131635"137636 /note="1310 and 9-bp target site duplication excised from between bases 137635 and 138973 CTGATGATGCCCCTAATGATTTTGGTAAAAATCATTAAGTTAAGGTGAACAACATGTGTGGAA TGTCATATGATCAAATGGTTTCGCGAAAAAATCAATAATCAGACAACAACAACATGTGTGGAA	source 1164500 /organism="Homo sapiens /mol_type="genomic DNA" /db_xref="taxon:9606"	7100 Loc		54 1	5720 5773	805 825	1 44 1	620 <800 

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DEFINITION
ACCESSION
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AC095698/c
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                                            Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Alder, J., Alyalebechi, V., Aoyagi, A., Aydeji, M., Baca, E., Baden, H., Balwin, D., Bandaranale, D., Barber, M., Barnstead, M., Benahmed, F., Blaiwalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Benahmed, F., Blaiwalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Benahmed, F., Bryant, M., Buhay, C., Burch, P., Burrell, K., Calderon, E., Chacko, J., Chavez, D., Chen, S., Chen, X., Chen, Y., Chen, Z., Chu, J., Claedand, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Claveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Claveland, C., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Delgado, O., Denson, S., Deramo, C., Durbin, K., Duval, B., Baves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flaggy, M., Gories, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratue, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Jackson, A., Jackson, L., Judyk, S., Hune, J., Idlebird, D., Jackson, A., Jackson, A., Louseged, H., Lozado, R.J., Lux, M., J., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Koyls, S., Muher, S., Martin, R., Martinez, E., Mawhiney, S., Miner, G., Minja, E., Montemayor, J., Moore, S., Mawhiney, S., Miner, G., Minja, E., Montemayor, J., Moore, S., Maykiney, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Paulsty, K., Reijly, R., Reijly, R., Reijly, R., Reijly, R., Reijly, R., Reige, F., Reige, 
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AC095698.6 GI:24817898
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP
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REILLUS DOTVEGICUS Clone CH230-9D13, WORKING DRAFT SEQUENCE.
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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SAG:apoptosis sensitivity gene
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
147 c 189 g 18
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Pred. No. 1.4e-14;
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                                                                                                              source
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On Nov 9, 2002 this sequence version replaced gi:23267899.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Rat Genome Sequencing Consortium.
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                                                                                                                                                                           are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that haprovided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 254832: contig of 254832 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_onorsets of 1 contigs. Gaps between the contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center clone name: CH230-9D13
------ Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 238918 bases at least Q40
Consensus quality: 241069 bases at least Q20
Consensus quality: 24204 bases at least Q20
Consensus quality: 242304 bases at least Q20
Estimated insert size: 243228; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 254832)
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Contact: hgsc-helpobcm.tmc.edu
------Project Information
Center project name: GDBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                 Location/Qualifiers
/mol_type="genomic DNA"
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                                                                                                              1. :254832
                                                                            organism="Rattus norvegicus
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misc_feature

clone="CH230-9D13"

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COMMENT
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TITLE
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Best Local
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 CCATCTGCAGGGTCCAGGTGATGGATGCCTGTCTTAG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-APR-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: Clonerequest@sanger.ac.uk On Apr 16, 2003 this sequence version replaced gi:29825605. Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence dat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Wellcome Trust Sanger Institute Center code: SC
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Mammalia; Eutheria; Rodentia;
(bases 1 to 120515)
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HTG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse DNA sequence from clone
                                                                                                                                                                                                                                                                                                                                                                                                   Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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ilarity 100.0%;
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1 58350 c 57410 g 64047 t
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clone_end:T7
site:EcoRI
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/note="wgs_contig"
complement(253801.
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253718. .254832
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2.8e-11;
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; Murinae; Mus.
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MEDLINE
PUBMED
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                                                               Matches
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Best Local Similarity
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TITLE
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                                                               35;
                                                                                                                                                                                                                                                                           Zabarovsky,E.R.
Zabarovsky,E.R.
Direct Submission
Submitted (16-MAY-2001) Microbiology
Submitted (16-MAY-1001) Microbiology
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 439)

Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F., Kvasha,S.M., Podowski,R.M., Matushkin,Y.G., Gyanchandani,A., Muravenko,O.V., Levitsky,V.G., Kolchanov,N.A., Protopopov,A.I., Kashuba,V.I., Kisselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R. NotI flanking sequences: a tool for gene discovery and verification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projectory from the RPCI-23 Mouse BAC Library constructed by the group of Pieter de Jong. Firther details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens genomic sequence surrounding NotI site, NB1-073R.
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                                                                                                                                                                                                                                                                                                                                                                                                              of the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
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CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGG 193
                  CGATACGTGCGCCATCTGCAGGGTCCAGGTGATGG 35
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                                                               Conservative
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                                                                                                                                          /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="MN1-073R"
a 161 C 146 g 68
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/clone_lib="RPCI-23"
25840 c 26441 g :
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/db_xref="taxon:10090"
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                                                              Score 35; DB; Pred. No. 3.2.
0; Mismatches
                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 10;
Pred. No. 1.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                             DB 9; L
. 3.2e-10;
                                                                                                                                               68 t
                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
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                                                                                             Length 439
                                                                                                                                                                                                                                                                           Tumorbiology Centre,
Box 280, Stockholm 171 77,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 120515;
                                                                                                                                               1 others
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                                                               Indels
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, clone
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                                                               Gaps
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Snoo

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ACCESSION
VERSION
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AC137264/c
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                                                                                                                                                                                                REFERENCE
AUTHORS
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                                       COMMENT
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                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                          Allen, C., Allen, H., Alsbrooks, S., Adms, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Allen, H., Alsbrooks, S., Allen, H., Barnstead, M., Benahmed, F., Baddwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Baddwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Berown, M., Canderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chu, J., Charber, M., Canderon, E., Cardenas, V., Carter, M., Carder, M., Canter, M., Divyal, B., Baves, K., Bayahn, A., Bacotto, M., Bugen, C., Ding, Y., Dinh, H., Divyal, K., Draper, H., Davyal, K., Canderon, D., Dersmo, C., Ding, Y., Dinh, H., Divyal, K., Draper, H., Davis, K., Canderon, A., Garner, T., Garza, M., Garcia, A., Garner, T., Garza, M., Garcia, A., Garner, T., Garza, M., Garrathe, Y., Havlak, P., Hawes, A., Henderson, N., Hernander, M., Hamilton, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernander, J., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernander, J., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernander, J., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernander, J., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernander, J., Liu, Y., Louiseged, H., Johnson, B., Johnson, R., Johnson
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HTG; HTGS_PHASE1; HTGS_DRF
Rattus norvegicus (Norway
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus clone CH230-66B6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Submitted (19-NOV-2002) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC137264
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                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                Rat Genome Sequencing Consortium
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                                                                                                                                                                                                                             (bases 1 to 264606)
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                                                                                                                                       Department
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KEYWORDS VERSION

BC011127.1 GI:15029807

ORGANISM

Mus musculus

Mus musculus (house mouse)

**FOCUS** 

ORIGIN

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RESULT 40
BC011127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
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ACCESSION
                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                          158502
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                                                                                                                                                                                                                                                              34 GGATGCCTGTCTTAGATGTCAAGCTGAAAACAAAC 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                table.
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                       Mus musculus ring finger protein IMAGE:4194107), complete cds.
BC011127
                                                                               BC011127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary Game herecome the continuous continuous data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                             GGATGCCTGTCTTAGATGTCAAGCTGAAAACAAAC 158468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be preserved.
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Center clone name: CH230-66B6
Center clone name: CH230-66B6
Center clone name: CH230-66B6
Assembly program: Phrap; version 0.990329
Consensus quality: 210747 bases at least Q40
Consensus quality: 214941 bases at least Q30
Consensus quality: 214941 bases at least Q30
Consensus quality: 214941 bases at least Q30
Consensus quality: 218032 bases at least Q20
Estimated insert size: 219724; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Baylor College of Medicine Center code: BCM
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ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="wgs_contig"
82489. .84829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66592. .67666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="wgs_contig"
53481 c 54146 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="CH230-66B6"
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66591: gap of unknown length
109095: contig of 42504 bp in length
109195: gap of unknown length
264606: contig of 155411 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Project Information
                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                  Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                        7,
                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                           4.9e-
                                                        mRNA (cDNA clone MGC:19076
                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                Length 264606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in length
                                                                                           ROD 16-APR-2003
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
MEDLINE
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TITLE
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                                                                CDS
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RIAUSDET, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D.,

Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K.,

Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L.,

Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L.,

Scheetz, T. E., Brownstein, M., Ugdin, T. B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J.,

Abramson, R. D., Mullahy, S. J., Bosak, S. A., McEwan, P. J.,

McKernan, K. J., Malek, J. A., Gunaratne, P. H., Richards, S.,

Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. M.,

Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y.,

Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D.,

Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M.,

Butterfield, Y. S., Krzywinski, M. I., Skalska, U., Smailus, D. E.,

Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M. A.

Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 24 Row: k Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Gwis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (25-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gibbs, R.A.
                                                                                                                  /note="synonym: SAG"
/db_xref="LocusID:19823"
                                                                                                                                                                         /gene="Rnf7"
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/tissue_type="Liver, normal. 5 month old male mouse."
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/lab_host="DH10B"
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/strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           location/Qualifiers
     product="Rnf7 protein"
                                                                                                                                                                                                                              note="Vector: pCMV-SPORT6"
                                                                                    db_xref="MGI:1337096"
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                                   start=1
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                                                                            RESULT 42
AF092877
DEFINITION
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Query Match
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Matches 32; Conserv
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OS Unidentified
PN JP 2001526063-A/1
PD 18-DEC-2001
PF 15-DEC-1998 JP 200
PR 19-DEC-1997 US
YI SUN
PC C12N15/09,A61K31/-
PC A61P39/06,
PC A61P3/00,C07K14/-
C12N5/10,C12Q1/68,
PC G01N33/50,G01N33/0
Strandedness: Double;
CC Topology: Linear;
CC /note = 'Mouse SAC
FH Key
FT CDS
FT mat peptide
1:
FT mat peptide
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                                                                                                                                                       11 GCCATCTGCAGGGTCCAGGTGATGGATGCCTG 42
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Mus musculus zinc RING finger protein SAG mRNA, complete cds. AF092877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sun,Y.
SAG:apoptosis sensitivity gene
Patent: JP 2001526063-A 1 18-DEC-2001;
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misc_feature 1. .114
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          note = 'Mouse SAG'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-1998 JP 2000525451
19-DEC-1997 US 60/068179,11-SEP-1998 US
                                                                                                                                                                                                                                                                           /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
224 c 287 g 32
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/db_xref="G1:19029808"
/db_xref="LocusID:19823"
/translation="MADVEDGEEPCVLSSHSGSAGSKSGGDKMFSLKKWNAVAMWSWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VECDTCAI CRVQVMDACLRCQAENKQEDCVVVWGECNHSFHNCCMSLWVKQNNRCPLC
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100.0%;
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                                                                                                                                                                                                         Score 32; DB 6; L; Pred. No. 2.6e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Duan, H., Tsvetkov, L.M., Liu, Y., Song, Y., Swaroop, M., Wen, R., Kung, H.F., Zhang, H. and Sun, Y.
Promotion of S-phase entry and cell growth under serum starvation by SAG/ROCZ/Rbx2/Hrt2, an E3 ubiquitin ligase component:
association with inhibition of p27 accumulation
Mol. Carcinog. 30 (1), 37-46 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          growth, but not for germination: in cell cycle regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sun, Y. Yeast homolog of human SAG/ROC2/Rbx2/Hrt2 is essential for cell
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SAG, a novel zinc RING finger protein that protects cells from apoptosis induced by redox agents
Mol. Cell. Biol. 19 (4), 3145-3155 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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ree Radical Biol. Med. 27, 193-202 (1999)
(bases 1 to 1140)
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                                                                                                                                                                                                                                                 /dev____358
                                                                                                                                                                                                                      /note="redox sensitive, metal binding; expression protects
cells from apoptosis induced by redox compounds"
                                                                             QQDWVVQRIGK"
                                                                                                  VECDTCAICRVQVMDACLRCQAENKQEDCVVVWGECNHSFHNCCMSLWVKQNNRCPLC
                                                                                                                                      /product="zinc RING finger protein SAG'
/protein_id="AAD25961.1"
/db_xref="GI:4588032"
                                                                                                                   translation="MADVEDGEEPCVLSSHSGSAGSKSGGDKMFSLKKWNAVAMWSWD
                                                                                                                                                                                                     codon_start=1
                                                                                                                                                                                                                                                                              /tissue_type="lung"
/dev_stage="6-8 weeks"
                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/strain="C57BL/6xCBA"
                                                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                            sex="female"
                                                                                                                                                                                                                                                                                                                                             db_xref="taxon:10090"
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  25.8%;
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S212P6446FB3.T0 CZECHII/Ei Mus
tagged site.
EV071691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parkway, St. Louis, MO 63108, USA 4 (bases 1 to 219370)
McPherson,J.D. and Waterston,R.H.
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McPherson, J.D. and Waterston, R.H. The sequence of Mus musculus clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus chromosome 13 clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: submissions@watson.wustl.ed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site:http://genome.wustl.edu/gsc/index.shtml
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/chromosome="13"
/clone="RP23-354J3"
a 45568 c 45395 g 666
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/mol_type="genomic DNA"
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                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 112321)
Birren,B., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-397H13
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
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The mosaic structure of variation in the laboratory mouse genome Nature 420 (6915), 574-578 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J
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Wade, C.M., Kulbokas, E.J. III,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        strain from which the particular read came. The these SNPs was estimated at approximately 98%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kerstin Lindblad-Toh
d Institute for Biomedical Research, Center for Genome
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/map="- 10 22-541 63463278-63462744"
/clone_lib="CZECHII/Ei"
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/mol_type="genomic DNA"
/strain="CZECHII/Ei"
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Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Liu,G.,
MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Raymond,C., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
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Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (20-DEC-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Dec 20, 2002 this sequence version replaced gi:17149550. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Research, 320 Charles Street, Cambridge, MA 02141, 3 (bases 1 to 112321)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                NOTE: This record contains 89 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
                                                                                                                                                                                                                                                              will be sequenced to completion. In the event the
                                                                                                                                                                                                                                                          the record is updated, the accession
                                                                                                                                                                                                                                                                                                                             However, it should not be assumed that this clone
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Center clone name: 397_H_13
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3 (barren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Gonde,S., Gord,S., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
Jones,C., Kamat,A., Karatas,A., Towins B., Lin,G.
                                                                                                                                                                                               Mammalia; Eutheria; Rodentia; Sciui 1 (bases 1 to 112321)
Birren,B., Nusbaum,C. and Lander,E. Mus musculus, clone RP23-397H13
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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3313: contig of 1176 bp
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35107: contig of 1194 bp
15207: gap of 100 bp
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35107: contig of 1201 bp
35107: contig of 1204 bp
16431: contig of 1204 bp
16531: gap of 100 bp
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135: gap of 100 bp
967: contig of 1176 bp
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REFERENCE COMMENT TITLE JOURNAL JOURNAL AUTHORS Research, 320 Charles Street, Cambridge, MA 02141, USA

Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Malthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zalnoun, J., Zembek, L., Zimmer, A. and Zody, M. MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Triglio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. * NOTE: This record contains 89 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will Submitted (20-DEC-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Dec 20, 2002 this sequence version replaced gi:17149550. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html Submitted (29-NOV-2001) Whitehead Institute/MIT Center for Genome Direct Submission Center project name: 3: Contact: sequence_submissions@genome.wi.mit.edu Web site: http://www-seq.wi.mit.edu Center code: WIBR Center: Whitehead Institute/ MIT Center for Genome Research preserved 1148 1248 2349 2449 2449 3512 3512 3612 4747 4847 6031 6131 -- Genome Center 1147: contig 1247: gap of 2348: contig 2448: gap of 3511: contig 3511: contig 4746: contig 4846: gap of 6130: gap of 6130: contig 7390: contig 397_H_13 L19615 f 100 bp g of 1184 bp i f 100 bp g of 1160 bp f 100 bp g of 1063 bp f 100 bp g of 1135 bp g of 1147 bp f 100 bp g of 1101 bp in length in in length in length in length length 43971 44071 45151 45251 46348 46448 47609 47709 48882 50341 50341 51645 51645 30135 30135 30135 31237 31337 32613 32613 33914 33914 33914 33914 33914 33914 33914 33914 33914 33914 33914 34108 36532 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 37702 17562 18751 18751 19913 20013 21200 21300 22463 22463 23721 23721 23721 23821 25006 26266 26266 26266 26266 26266 26262 27629 27629 27629 7391 8578 8678 9938 10038 11193 11293 16235 16335 17462 13819 15003 15103 12455 12555 13719 52828: 52928: 50340: 51544: 51644: 48981 48881 38967 31336 40235 3261 44070 43970 40335 16334 gap of contig gap of contig gap of gap of contig gap of contig gap of contig gap of contig gap of gap of contig gap of contig gap c gap of contig gap of gap of contig gap of contig gap of contig gap gap gap gap gap gap gap of contig gap of contig gap of contig gap of contig gap gap gap contig contig contig contig contig contig of 1259 100 bp of 1204 100 bp of 1184 100 bp 100 bp of 1173 100 bp 100 bp of 1161 of 1157 100 bp 100 bp 100 bp 100 bp of 1170 100 bp of 1194 100 bp of 1160 100 bp of 1163 100 bp 100 bp of 1163 100 bp of 1158 of 1155 100 bp of 1162 100 bp 100 bp of 1179 100 bp of 1224 100 bp of 1201 100 bp of 1102 of 1160 bp in length 100 bp of 1146 bp in length 100 bp of 1185 of 1162 100 bp of 1089 100 bp 100 bp of 1127 100 bp of 1132 100 bp of 1184 100 bp of 1164 of 1260 100 bp 100 bp of 1176. bp 100 bp of 1187 100 bp 100 pp đđ ģ ģ đđ ģ đđ å, ďď ģ ď ď đđ đđ đđ ď ď đđ ģ đđ ď ď ď ď ģ bp in length đq bp in length ď ģ đđ ďq ďq đđ in length in length in 'n 'n 'n 'n ä 'n ij 'n 'n 'n ä ij in length ä in length ij in length ij in length H ä 'n ä ä ij in in length ij חו in length length

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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                                                                          wirren,B., Linton,L., Nusbaum,C. and Lander,E. Mus musculus, clone RP23-200C17
                                                                                                                                                                                                                                                                                                                                                          AC118192.1 GI:20147957
HTG; HTGS PHASE2; HTGS DRAFT; HTGS FULLTOP
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Mus musculus clone RP23-200C17,
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NCE, 10 ordered
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                                                                                                                                            Gardyna, S.,
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32182
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730
751
                                             /note="assembly_fragment"
730. .750
 /note="assembly_fragment"
                          note="assembly_fragment"
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ACCESSION

KEYWORDS VERSION

TITLE

_lib="RPCI-23 Female

Mouse

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Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Research, 320 Charles Street, Cambridge, MA 021
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (14-APR-2002) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: Plasmid; n/a; 100% of reads Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731

Consensus quality: 184259 bases at least Q40 Consensus quality: 185710 bases at least Q30 Consensus quality: 185710 bases at least Q20 Insert size: 194000; agarose-fp Insert size: 194000; agarose-fp Quality coverage: 7.4 in Q20 bases; agarose-fp Quality coverage: 7.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence will be replaced
This sequence will be replaced
by the finished sequence as soon as it is available
the accession number will be preserved.

1 629: contig of 629 bp in length
630 729: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It curreconsists of 10 contigs. Gaps between the contigs are represented as runs of N. The order of the pris believed to be correct as given, however the soft the gaps between them are based on estimates to the soft the gaps between them are based on estimates to the soft the gaps between them are based on estimates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Whitehead Institute/ MIT Center for Genome
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/mol_type="yearon:10090"
/db_xref="taxon:10090"
                                                                                                                                                3 187353: contig
Location/Qualifiers
                                                                              organism="Mus musculus"
                                                                                                                                                                   7008: gap of 100 bp
14434: contrig of 7426 bp in
14534: gap of 100 bp
32181: contrig of 17647 bp in
32281: gap of 100 bp
51167: contrig of 18886 bp in
51267: gap of 100 bp
72870: contrig of 21603 bp in
72970: gap of 100 bp
149992: contrig of 77022 bp in
187353: contrig of 37261 bp in
                                                                                                                                                                                                                                                                                           750: contig of 21 bp in length
850: gap of 100 bp
3212: contig of 2362 bp in length
3312: gap of 100 bp
6908: contig of 3556 bp in length
7008: gap of 100 bp
14434: contig of 7426 bp in length
14534: gap of 100 bp
32181: gap of 100 bp
32181: gap of 100 bp
51167: gap of 100 bp
51167: gap of 100 bp
51267: gap of 100 bp
51267: gap of 100 bp
72870: contig of 21603 bp in length
                                                     _type="genomic DNA"
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AC119145
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                                                                                                                                                                                                                                   Rattus norvegicus chromosome 1 SEQUENCE, 10 unordered pieces.
                                                                                                                                                                                                                                                                                                                                             Biotechnology, Beutenberstr.
3 (bases 1 to 148290)
Taenzer, S. and Platzer, M.
                                                                                                                                                                                                                                                                                                                                                                               Submitted (25-APR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena, Thuringia 07745, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Taenzer, S., Monti, J., Gloeckner, G., Huebner, N. and Platzer, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_DRAFT Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                           Submitted (11-JUN-2002) Genome Analysis, Institute of Molecular
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Taenzer, S. and Platzer, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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Center project name: rA08
Center clone name:RD32-4G14
Center clone name:RD32-4G14
Sequencing vector: pUC18; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 140730 bases at least Q40
Consensus quality: 143676 bases at least Q30
Consensus quality: 143676 bases at least Q30
Quality coverage: 8.49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 148290)
                                                                                                                                                                             Web site: http://genome.imb-jena.de/
Contact: gscj-submit@genome.imb-jena.de
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7009 ..14434
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34855 c 36129 g 54836 t
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100.0%; Pr/
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Pred. No.
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DMOSOME 1 Clone RP32-4G14, WORKING DRAFT
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                                                                                                                                                                                                                                                                                      Thuringia 07745,
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REFERENCE
AUTHORS
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AC118520/c
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                                                                                                                                                                                                                                                                                                                                                                             17405
                                                                                                                                                                                                                189541 bp DN:
Rattus norvegicus clone CH230-304J21,
***, 2 unordered pieces.
AC118520
1 (bases 1 to 189541)
Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano,
                                                                                                                      HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED Rattus norvegicus (Norway rat)
Rattus norvegicus
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AC118520.4 GI:25138134
                                                                Rattus.
                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
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This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                             TGCGCCATCTGCAGGGTCCAGGTGATGGAT 17434
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/clone lib="RPCI-32 BAC Library"
31830 c 31870 g 41911 t 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/db_xref="taxon:10116"
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112270: gap of unknown length
119805: contig of 7535 bp in length
119905: gap of unknown length
137949: contig of 18044 bp in length
138049: gap of unknown length
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146603: gap of unknown length
148200: contig of 1687 bp in length
tion/Qualifiers
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107588: contig of 16815 bp in length
107688: gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.4e-07;
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                                                                                                                                                                                                                                                SEQUENCING
                                                                                                                                                                                                                                                                      linear
    Adams,C., Alder,J
nguiano,D.,
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                                                                                 Euteleostomi;
; Murinae;
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PROGRESS
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Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Bhay, C., Burch, P., Burrell, K., Calderon, E., Chu, J., Clare, I., Cher, C., Cher, C.
AL Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 20, 2002 this sequence version replaced gi:23914484. On Nov 20, 2002 this sequence version replaced gi:23914484. On Nov 20, 2002 this sequence version replaced gi:23914484. On Nov 20, 2002 this sequence version replaced gi:23914484. On Nov 20, 2002 this sequence version replaced gi:23914484. On Nov 20, 2002 this sequence years assembled using Atlas and whole genome shotgun sequence contigy reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (18-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 189541)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Worley, K.C.
Direct Submission
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TITLE JOURNAL REFERENCE

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COMMENT

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DEFINITION
ACCESSION
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                                                                                                                                                                                                                                                                                     RESULT 50
AC135657
LOCUS
                                                                                                                                           SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                        93758 GGACTGTGTTGTGGTCTGGGGAGAATGTAA 93729
                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 GGACTGTGTTGTGGTCTGGGGAGAATGTAA 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30;
                                                                                                                                       HTG; HTGS PHASE2; HTGS DRAFT; HTGS FULLTOP Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          table.
Muzny, D. Marie., Metzker, M. Lee., Al Allen, C., Allen, H., Alsbrooks, S.,
                                                                                                                                                                                                              AC135657
AC135657.2 GI:25073392
                                                                                                                                                                                                                                                            AC135657 198756 bp DNA linear
Rattus norvegicus clone CH230-416B17, WORKING DRAFT
                                                                         Rattus.
                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49137
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                                              (bases 1 to 198756)
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center clone name: CH230-304J21
center clone name: CH230-304J21
center clone name: CH230-304J21
center clone name: Phrap; version 0.990329
Assembly program: Phrap; version 0.990329
consensus quality: 173927 bases at least Q30
consensus quality: 175964 bases at least Q30
consensus quality: 176952 bases at least Q30
consensus quality: 176952 bases at least Q30
stimated insert size: 178045; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: hgsc-help@bcm.tmc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188515
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clone_end:T7"
a 39834 c 38226 g 5053
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/note="clone_boundary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 188414: contig of 188414 bp in length
5 188514: gap of unknown length
5 189541: contig of 1027 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone="CH230-304J21"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.2%; Score 30; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Project Information
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                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; I
                        Abramzon, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 189541;
                           Adams, C., Alder, J.,
                                                                                                                                                                                                                                                                                          HTG 19-NOV-2002
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Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, B., Baden, H., Baldein, H., Bandaricad, K., Bandaric, F., Barnescad, K., Bandaric, B., Baves, K., Bandaric, F., Bandari
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REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

Search completed: November

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Job time : 825.044 secs

JOURNAL REFERENCE

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176453 AGATGTCAAGCTGAAAACAAACAAGAGGAC 176482
                                          47
                                                                                   30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).

* NOTE: This is a 'working draft' sequence. It currently

* Consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              table
                                        AGATGTCAAGCTGAAAACAAACAAGAGGAC 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                               51425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: KBVZ
Center clone name: CH230-416B17
Center clone name: CH230-416B17
Center clone name: CH230-416B17
Center clone name: CH230-416B17
Center clone name: Phrap; version 0.990329
Consensus quality: 187507 bases at least Q40
Consensus quality: 189483 bases at least Q20
Consensus quality: 199529 bases at least Q20
Estimated insert size: 192210; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                                                                                                                                                                                                 complement (191645. .1 /note="clone_boundary clone_end:T7
                                                                                                                                                                                        /note="wgs_end_extension clone_end:T7" 44460 c 43469 g 51990
                                                                                                                                                                                                                                                       end_sequence:BZ197451"
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/db_xref="taxon:10116"
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                                                                                <u>.</u>
                                                                                                     Score 30; Pred. No.
                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                   .192594)
                                                                                                                         DB 2;
                                                                                                       6.5e-07
                                                                                                                                                                                            7404 others
                                                                                                                         Length 198756;
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